



OIPE

RAW SEQUENCE LISTING

DATE: 01/24/2002

PATENT APPLICATION: US/10/006,041

TIME: 14:23:28

Input Set : A:\Seq\_List\_for\_P2830PlC8.wpd

Output Set: N:\CRF3\01242002\J006041.raw

3 <110> APPLICANT: Baker, Kevin P.  
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 5 Desnoyers, Luc  
 6 Eaton, Dan I.  
 7 Ferrara, Napoleone  
 8 Fong, Sherman  
 9 Gao, Wei-Qiang  
 10 Goddard, Audrey  
 11 Godowski, Paul J.  
 12 Grimaldi, Christopher J.  
 13 Gurney, Austin L.  
 14 Hillan, Kenneth J.  
 15 Pan, James  
 16 Paoni, Nicholas F.  
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Does Not Comply  
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FYI →

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Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.



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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,041

DATE: 01/24/2002

TIME: 14:23:29

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Output Set: N:\CRF3\01242002\J006041.raw

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\01242002\J006041.raw

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L:6172 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:98  
L:6884 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:105  
L:6887 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:105  
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L:6900 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:106  
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L:6913 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:107  
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L:6926 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:108

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Input Set : A:\Seq\_List\_for\_P2830PlC8.wpd

Output Set: N:\CRF3\01242002\J006041.raw

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 .:7092 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:114  
 .:7095 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:114  
 .:7473 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:119  
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 .:20824 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 .:20939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:377  
 .:22554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:422

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Leu Glu Asn Tyr Phe	Ser Leu Leu Asn Glu	Lys Ala Thr Asn Val	
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Pro Phe Val Leu Ile	Ala Thr Gly Thr Val	Ile Ile Leu Leu Gly	
65	70	75	
Thr Phe Gly Cys Phe	Ala Thr Cys Arg Ala	Ser Ala Trp Met Leu	
80	85	90	
Lys Leu Tyr Ala Met	Phe Leu Thr Leu Val	Phe Leu Val Glu Leu	
95	100	105	
Val Ala Ala Ile Val	Gly Phe Val Phe Arg	His Glu Ile Lys Asn	
110	115	120	
Ser Phe Lys Asn Asn	Tyr Glu Lys Ala Leu	Lys Gln Tyr Asn Ser	
125	130	135	
Thr Gly Asp Tyr Arg	Ser His Ala Val Asp	Lys Ile Gln Asn Thr	
140	145	150	
Leu His Cys Cys Gly	Val Thr Asp Tyr Arg	Asp Trp Thr Asp Thr	
155	160	165	
Asn Tyr Tyr Ser Glu	Lys Gly Phe Pro Lys	Ser Cys Cys Lys Leu	
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Glu Asp Cys Thr Pro	Gln Arg Asp Ala Asp	Lys Val Asn Asn Glu	
185	190	195	
Gly Cys Phe Ile Lys	Val Met Thr Ile Ile	Glu Ser Glu Met Gly	
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 Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile  
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 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln  
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 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser  
                   65                  70                  75  
  
 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro  
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 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu  
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 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

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 <223> Casein Kinase II Phosphorylation Site.

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 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaa 1508

<210> 10  
 <211> 319  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> sig\_peptide  
 <222> 1-17  
 <223> Signal Peptide  
  
 <220>  
 <221> misc\_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212  
 <223> N-myristoylation Sites.

<220>  
 <221> misc\_feature  
 <222> 39-42  
 <223> Glycosaminoglycan Attachment Site.

<220>  
 <221> TRANSMEM  
 <222> 136-152  
 <223> Transmembrane Domain

<220>  
 <221> misc\_feature  
 <222> 161-163, 187-190 and 253-256  
 <223> N-glycosylation Sites.

<400> 10  
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 Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
 20 25 30  
 Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
 35 40 45  
 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
 50 55 60  
 Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
 65 70 75  
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
 80 85 90  
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
 95 100 105  
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
 110 115 120  
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
 125 130 135  
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
 140 145 150  
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
 155 160 165  
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys  
 170 175 180  
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
 185 190 195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315

Pro Lys Ala Val

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
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 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggcggg 100  
 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200  
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
 gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
 agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800  
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
 ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000  
 aacctgtttg agagcacgat ccgcattcctg ggggggctcc tgagtgccta 1050  
 ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100  
 atcggctaata gcctgccttc agaacaccat ccaagattcc ttactcggat 1150  
 gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200  
 cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
 cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
 caataccac agtggcctct tcaccacact gggcgtattc acgctgggag 1400  
 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450  
 ggggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500  
 tgtcagaacg cacctgctgc ggcactccga gccagtaag ctacaccttg 1550  
 tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600  
 tgcttctctgc cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650  
 cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
 accggcagat ggagacgggg ctgagtcccc agatcgtgca cttcaacctt 1750  
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 caacctgctg cggccagaga ccgtggagag cctgtttctac ctgtaccgag 1850  
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900  
 ttcagccgat tcacacgggt cccctcggtt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
 tcctggggga gacgtcaag tatctgttct tgctcttctc cgatgacca 2050  
 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150  
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aagggcccac 2200  
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250  
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300  
 cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
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 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450  
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctcgtgaagc 2500  
 ctcagatgtc cccaatcaa gggctctggag gggctgccgt gactccagag 2550  
 gcctgaggct ccagggtctg ctctggtgtt tacaagctgg actcagggat 2600  
 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
 tagctcagg gccctccag tggaatgggt ctttccggtg gagataaaag 2700  
 ttgatttgct ctaaccgcaa 2720

<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
     1                    5                    10                    15  
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
                     20                    25                    30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro  
                     35                    40                    45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
                     50                    55                    60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
                     65                    70                    75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
                     80                    85                    90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
                     95                    100                    105



Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe			

395					400					405				
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
				680					685					690

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgcgt aggcccgga ggccgggccg gccgggctgc gagcgctgc 50  
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
 cccaccgcct ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400  
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
 gcaccacatc tacgtgtca accaggtgga ccacttcagg ttcaaccggg 500  
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550  
 attgcatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
 tggctttcct gaggtgtggc ccttcacgt ggctccccg gagctccacc 650  
 ctctctacca ctacaagacc tatgtcggcg gcactcctgct gctctccaag 700  
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggtgtggg 750  
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800  
 ttttcgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850  
 catgaccag cctggcgaa gagggaccag aagcgcatcg cagctcaaaa 900  
 acaggagcag ttcaaggtgg acaggaggagg aggcctgaac actgtgaagt 950  
 accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000  
 gtctcaaca tcattgtgga ctgtgacaag accgccacac cctggtgcac 1050  
 attcagctga gctggatgga cagtaggaa gcctgtacct acaggccata 1100  
 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150  
 atgtggagt gccaggacca agacagcaag ctacgcaatt gcagccacc 1200  
 ggccgccaag gcaggcttg gctgggccag gacacgtggg gtgcctggga 1250  
 cgctgcttg catgcacagt gatcagagag aggtgtgggt gtgtcctgtc 1300  
 cgggacccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350  
 ccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450  
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
                   20                  25                  30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                   35                  40                  45  
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
                   50                  55                  60  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
                   65                  70                  75  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
                   80                  85                  90  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
                   95                  100                  105  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
                   110                  115                  120  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
                   125                  130                  135  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140										145					150				
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp					
				155					160					165					
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala					
				170					175					180					
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His					
				185					190					195					
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His					
				200					205					210					
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly					
				215					220					225					
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu					
				230					235					240					
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe					
				245					250					255					
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg					
				260					265					270					
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly					
				275					280					285					
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu					
				290					295					300					
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp					
				305					310					315					
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser								
				320					325										

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
 gcgaacgctt cgaggagtcc tgg 23

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-24  
<223> Synthetic construct

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgacagcaag ccagcccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaat<sup>1</sup>at gtctttataa 450  
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg cggcccgcta ggccagtgcg ccgcgcgctc ccccgaggc 200

cccgccccgc agcatggagc caccggagc cggcgggggc cgcgcgagc 250

cgccgctgtt gctgccgctc tcgctgtag cgctgctgc gctgctggga 300

ggcgccggcg gcggcgccgc cgcggcgctg cccgcgggt gcaagcacga 350

tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tggtgtgcag cagcctggaa ctgcgcagg tctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500

gaagaatggc tcattttctg ggtaagtct cttgaaaga ttggacctcc 550

gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600

tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650

agacatattt cgaggactca ccaatctggg tcggctaaac ctttcgggga 700

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cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800

gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850



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 cgtgggaata atacaggac tgtggatatt gtggtattag agagtctgc 1250  
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 gaaattacat ttataactg cagtgggtata aatgcaaata tactattggt 2300

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 atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650  
 ctaatggaac cacatttttt tcaacttagct ttctgtgggc atgtgtaatt 2700  
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 ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850  
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
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     1                    5                    10                    15  
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
                     20                    25                    30  
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
                     35                    40                    45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
                     50                    55                    60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
                     65                    70                    75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
                     80                    85                    90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	95	100	105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	110	115	120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	125	130	135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	140	145	150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	155	160	165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	170	175	180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	185	190	195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	200	205	210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	215	220	225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	230	235	240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	245	250	255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	260	265	270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	275	280	285
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	290	295	300
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	305	310	315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	320	325	330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	335	340	345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	350	355	360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	365	370	375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro			

380										385					390				
Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe					
				395					400					405					
Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
				410					415					420					
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
				425					430					435					
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu					
				440					445					450					
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu					
				455					460					465					
Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys					
				470					475					480					
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu					
				485					490					495					
Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala					
				500					505					510					
Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
				515					520					525					
Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile					
				530					535					540					
Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met					
				545					550					555					
Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly					
				560					565					570					
Leu	Ser	Asp	Tyr	Gly	Arg	Arg	Asp	Pro	Glu	Gly	Asn	Leu	Asp	Lys					
				575					580					585					
Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
				590					595					600					
Ala	Leu	Lys	Val	Cys	Tyr	Ile	Leu	Gln	Ser	Phe	Lys	Thr	Ile	Tyr					
				605					610					615					

Ser

<210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24

<223> Synthetic construct

<400> 25  
gaggactcac caatctgggt cggc 24

<210> 26  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 26  
aactggaaag gaaggctgtc tccc 24

<210> 27  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 27  
gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28  
<211> 683  
<212> DNA  
<213> Homo sapiens

<400> 28  
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gcagaggctt cgtgacggag ttatcagaga cattgaga<sup>11</sup>gg caaatcggga 150  
aaaaagaaaa cattcgtctt ttgggagaac agattat<sup>11</sup>ttt gactgagcaa 200  
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250  
atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300  
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350  
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400  
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450  
tttgaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500  
tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600  
 atgacgaagc cacgagaaca tcgacctcag aaggactgga ggaaggtgaa 650  
 gtggaggagg agacgtcct gatcgtcgaa tcc 683

<210> 29  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-21  
 <223> Signal peptide.

<400> 29  
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 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
                   20                  25                  30  
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
                   35                  40                  45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
                   50                  55                  60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
                   65                  70                  75  
 Lys Gly Ser Gln Lys Ser  
                   80

<210> 30  
 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
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 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaacccg 150  
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200  
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250  
 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtcgg tggctagcgt 300  
 gggcgccctg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350  
 tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
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ctatgcggcc ctcttctgcc tctcggcctc catcatctac cccaccacct 500  
atgtccagtt cctgtccac gccggttcgc gggaccacgc catcgccgcc 550  
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gaccgcccac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050  
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actctcccaa gaggtcccg ttccctctcc aacctcttg ttcttcttgc 1150  
ccgagttttc tttatggagt acttctttcc tccgcctttc ctctgttttc 1200  
ctcttctgt ctccctccc tcccacctt ttctttcctt cccaattct 1250  
tgcaactctaa ccagtctctg gatgcatctt ctctctccc ttctctctg 1300  
ctgtttcctt cctgtgttg tttgttgccc acatcctgtt ttcacccctg 1350  
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tcttatctgc ctgttttgca agcaccttct cctgtgtcct tgggagcct 1650  
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ggccctcttt ctcccagtg aggaaggtgt gcagtgtact tccccttaa 1900

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950  
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000  
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050  
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 cccaactatt ctctgtggta tgaaaaag 2128

<210> 31  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
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 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val  
 35 40 45  
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
 50 55 60  
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
 80 85 90  
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
 95 100 105  
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
 110 115 120  
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
 125 130 135  
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
 140 145 150  
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
 155 160 165  
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
 170 175 180  
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
 185 190 195  
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
 200 205 210



Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
				305					310					315	
His	Leu	Val	Phe	Val	Lys	Val									
				320											

<210> 32  
 <211> 3680  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 tcacctgggc ctcccaaagt gctgggatta caggcatgag ccactgacgc 150  
 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200  
 taaacattgg gcactacagt gaccaaaca gactgaattc cccaagagcc 250  
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
 ttattactca ctatgactaa gggtcacaaa tggggtacgt tgatggagag 350  
 tgatttgta agagactaca gagggaggac agactaccaa gaggggggcc 400  
 aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450  
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 cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550  
 ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600  
 aagggaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650  
 gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700

gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750  
 tgggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800  
 agaaggtgtg ggggttttgg ttccatcttg ccgagtctgc cggaatgtgg 850  
 atgggaagac caagaggagg agcaaggggc agaggggaag ggaatcttaa 900  
 agaagtcctg gatgccacac tcttcttctt tctctctctt cctctctctc 950  
 agaggtctca ctctgtgttc ttcatttctt gccctgcctc catctctctt 1000  
 ggggtgctggg aaagtggagg attagctgaa gttttgcttc tcggggcctg 1050  
 tctgaatctc cattgctttc tgggaggaca taattcacct gtcctagctt 1100  
 cttatcatct tacatttccc tgtagccact gggacatatg tgggtgttct 1150  
 tcttagctcc tgtctctcc tcatgccttt gctgggtatg ggcatgttag 1200  
 ggggaaggtc attgctgtca gaggggcact gactttctaa tgggtgttacc 1250  
 caaggtgaat gttggagaca cagtcgcgat gctgccaag tcccggcgag 1300  
 ccctaactat ccaggagatc gctgcgctgg ccaggtcctc cctgcatggg 1350  
 atgcagcccc tcccatgttt ctggccactt tgtcctttct cctcccgttt 1400  
 gcacatccct ttggaactgt ttctgtgag tacatgctgg ggtctccct 1450  
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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
			335											

<210> 34  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct

<400> 34  
 tgtcctttgt cccagacttc tgtcc 25

<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 35  
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

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<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

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ccatctgttt tctctaatac acgacagatt cctttcagac aggacaactg 150

tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250

caatctattc ttgccacatc aagggattgt tattccttta aaaaaaacc 300

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caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
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ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195



Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
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 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
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 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
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 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
 aatgcagtga ttcttttctca ctactatctg tattgtggaa tgcacaaaat 1500  
 tgtgtagggt ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550  
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
 <211> 263  
 <212> PRT  
 <213> Homo sapiens

<400> 43  
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 1 5 10 15  
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 20 25 30  
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
 35 40 45  
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
				65					70					75					
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
				155					160					165					
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
				170					175					180					
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
				185					190					195					
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
				200					205					210					
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
				215					220					225					
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala					
				230					235					240					
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
				245					250					255					
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu												
				260															

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 45  
gggaactgct atctgatgcc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 46  
caggatctcc tcttgcatc tgcagc 26

<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgaac cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

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ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700  
ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750  
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 <212> PRT  
 <213> Homo sapiens

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 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
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 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
 80 85 90  
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
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 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
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 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
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 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
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Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
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Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
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Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
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Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
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Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
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 <212> DNA  
 <213> Homo sapiens

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 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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                   20                  25                  30  
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
                   35                  40                  45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly



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				95					100					105					
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				110					115					120					
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val					
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Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile					
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Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
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Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg
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 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

<400> 54

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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
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Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
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<212> DNA  
<213> Homo sapiens

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a 2401

<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

Met	Ser	Ser	Asn	Lys	Glu	Gln	Arg	Ser	Ala	Val	Phe	Val	Ile	Leu
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Phe	Ala	Leu	Ile	Thr	Ile	Leu	Ile	Leu	Tyr	Ser	Ser	Asn	Ser	Ala
				20					25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens



<400> 57

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<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
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Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr	Asn 275	Lys Thr Arg Phe	Leu 280	Leu Ser Asn Leu	Leu 285
Ile Asp Thr Thr	Ser 290	Glu Glu Asp Ser	Gly 295	Thr Tyr Arg Cys	Met 300
Ala Asp Asn Gly	Val 305	Gly Gln Pro Gly	Ala 310	Ala Val Ile Leu	Tyr 315
Asn Val Gln Val	Phe 320	Glu Pro Pro Glu	Val 325	Thr Met Glu Leu	Ser 330
Gln Leu Val Ile	Pro 335	Trp Gly Gln Ser	Ala 340	Lys Leu Thr Cys	Glu 345
Val Arg Gly Asn	Pro 350	Pro Pro Ser Val	Leu 355	Trp Leu Arg Asn	Ala 360
Val Pro Leu Ile	Ser 365	Ser Gln Arg Leu	Arg 370	Leu Ser Arg Arg	Ala 375
Leu Arg Val Leu	Ser 380	Met Gly Pro Glu	Asp 385	Glu Gly Val Tyr	Gln 390
Cys Met Ala Glu	Asn 395	Glu Val Gly Ser	Ala 400	His Ala Val Val	Gln 405
Leu Arg Thr Ser	Arg 410	Pro Ser Ile Thr	Pro 415	Arg Leu Trp Gln	Asp 420
Ala Glu Leu Ala	Thr 425	Gly Thr Pro Pro	Val 430	Ser Pro Ser Lys	Leu 435
Gly Asn Pro Glu	Gln 440	Met Leu Arg Gly	Gln 445	Pro Ala Leu Pro	Arg 450
Pro Pro Thr Ser	Val 455	Gly Pro Ala Ser	Pro 460	Lys Cys Pro Gly	Glu 465
Lys Gly Gln Gly	Ala 470	Pro Ala Glu Ala	Pro 475	Ile Ile Leu Ser	Ser 480
Pro Arg Thr Ser	Lys 485	Thr Asp Ser Tyr	Glu 490	Leu Val Trp Arg	Pro 495
Arg His Glu Gly	Ser 500	Gly Arg Ala Pro	Ile 505	Leu Tyr Tyr Val	Val 510
Lys His Arg Lys	Gln 515	Val Thr Asn Ser	Ser 520	Asp Asp Trp Thr	Ile 525
Ser Gly Ile Pro	Ala 530	Asn Gln His Arg	Leu 535	Thr Leu Thr Arg	Leu 540
Asp Pro Gly Ser	Leu 545	Tyr Glu Val Glu	Met 550	Ala Ala Tyr Asn	Cys 555
Ala Gly Glu Gly	Gln Thr Ala Met	Val Thr Phe Arg	Thr Gly Arg		

560										565					570				
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln					
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Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Ser	Gln	Pro	Asp				
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His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile					
				605					610					615					
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg					
				620					625					630					
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys					
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Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile					
				650					655					660					
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly					
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Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu					
				680					685					690					
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr					
				695					700					705					
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr					
				710					715					720					
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met					
				725					730					735					
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr					
				740					745					750					
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys					
				755					760					765					
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His					
				770					775					780					
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn					
				785					790					795					
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr					
				800					805					810					
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro					
				815					820					825					
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg					
				830					835					840					
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro					
				845					850					855					

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu		950	955	960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His		965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly		980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro		995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys		1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg		1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro		1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu		1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp		1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly		1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr		1100	1105	1110
Pro	Pro	Leu	Thr	Ile												1115		

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 <212> DNA  
 <213> Artificial

<220>  
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<222> 1-25  
<223> Synthetic construct.

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<210> 60  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 60  
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<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-42  
<223> Synthetic construct.

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<210> 62  
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<212> DNA  
<213> Homo sapiens

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<223> unknown base

<400> 62  
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 catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950  
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatggtga 1050  
 cactgtccat ggggggtgctg cagtgcgaacc tgcttgctaa cgtgtccact 1100  
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150  
 cgggattggt ggaaattatg acgggactgg ccggttccct caggggctgg 1200  
 aggatgtgtc cacatacca gtcctgatag aggagttgct gagtcgtasc 1250  
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350  
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactccac 1400  
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
 gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500  
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
 tgctgacaca gtcggtcccc gcagaggtea ctgtggcaaa gcctcacaaa 1600  
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
 cacatggaaa a 1661

<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro 275 280 285		
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu 290 295 300		
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly 305 310 315		
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu 320 325 330		
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg 335 340 345		
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp 350 355 360		
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr 365 370 375		
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu 380 385 390		
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg 395 400 405		
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val 410 415 420		
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser 425 430 435		
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val 440 445 450		
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala 455 460 465		
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro 470 475 480		
Thr Phe Thr Gln Trp Leu Cys 485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 65  
 gtcacacaca gctctggcag ctgag 25

<210> 66  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 66  
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67  
 <211> 1564  
 <212> DNA  
 <213> Homo sapiens

<400> 67  
 tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50  
 aacaccacaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100  
 ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150  
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
 gcccatgcc a gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
 agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
 atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450  
 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
 acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
 tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650  
 atcggcacia gatgctcagc tagatgggct ggtgtgggtg ggtcaaggcc 700  
 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
 ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
 ctctttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850  
 aagaggggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt 900  
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
 ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
 cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050  
 ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100  
 gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150  
 ctacgcccc accccagctc cagccctgag gacagctctg atgggagagc 1200  
 tgggccccct gagcccactg ggtcttcagg gtgcactgga agctgggtgt 1250  
 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
 ctctgctgcc ggtccctca cctgcacttg aggggtctgg gcagtccttc 1350  
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
 gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450  
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
 tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550  
 ttttatttct ctca 1564

<210> 68  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
 1 5 10 15  
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
 20 25 30  
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
 35 40 45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
				170					175					180	

Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50  
 agttcatagg gtcttgggtc cccgaaccag gaagggttga gggaacacaa 100  
 tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggctctccc 150  
 tccctttgca tccccacccc tccgggcttt gcgtcttctt ggggaccccc 200  
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250  
 tgctctact ggccgcggtg ctgatggttg agagctcaca gatcggcagt 300  
 tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350  
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550  
 gcatgtgctg cccagtagcc cgctgcaata atggcatctg tatcccagtt 600  
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gaccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800  
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
gtaccaaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
catggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100  
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350  
ttatacaaat aacctacatg ccagatttct attcaacgtt agagtttaac 1400  
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450  
gctaaacaag aatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttgg 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac ttttttttca aaattttagt tttacctgta attaataaga 1700  
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750  
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aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaat tttaaagatgt ccaatatatg tgggaaaaga 1900  
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150  
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 tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
 tgctgagatc ctcaaataat ctcaatttca ggagggttca caaaatgtac 2300  
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 ctttattgcc aaagggttag tttcggtttt ctgcagccat tgcggttaaa 2450  
 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
 accacagttt cttaaattctt tgaaaccact ttactacttt ttttaaactt 2550  
 aactcagttc taaatacttt gtctggagca caaaacaata aaaggttatc 2600  
 ttatagtcgt gactttaaac tttttagtag cacaattcac tttttagttt 2650  
 tcttttactt aaatcccatc tgcagtctca aatttaagtt ctcccagtag 2700  
 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
 tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800  
 caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850  
 tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900  
 atataacaat tattatatatt acaatttggg ttctgcaata tttttcttat 2950  
 gtccaccctt ttaaaaatta ttatttgaag taattttatt acaggaaatg 3000  
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
 gcagaatata ttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
 taagataaaa tctattaaat ttttctctc taaaaactga aaaaaaaaaa 3150  
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu  
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 Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
 20 25 30  
 Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
 35 40 45



Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
 65 70 75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
 80 85 90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
 95 100 105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
 110 115 120  
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
 155 160 165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
 170 175 180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
 200 205 210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 230 235 240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
 245 250 255  
 Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
 tctcaatctg ctgacctgt gatccgctg accttgtaac ccacctacct 50  
 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100  
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250  
atatatttagt aattcatatg ttttagatta taggttttaa cataacttgtg 300  
aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
ggatttggtc ttttatcccc cttttaaagt catccgtcct tggctcagga 400  
tttgagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
tttgaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
ctcaagcccc caacatccca gtcctcagtc ctcaagtcac ttgacttcaa 600  
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
agcaccagag ccaggcagtc actgttcctc ctcttggtt ggagtccttt 700  
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800  
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
ataccccag cttctaagat ccagcttct gcagtggaaa tgcctggttc 900  
agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950  
cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000  
aatcagattc ccacagctt gtattcgaag tctttaagt agcctttgaa 1050  
tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100  
ccgtcattac ctctgcagt ctgacaagct catcactgaa ttctgctagt 1150  
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200  
cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
tgaatggaca tgggtggtgg cgaagtcagc agacactaga cagtaagtat 1300  
agcagcaagc tactcttgtc atggctggtg ccaaccaaac agaggaagag 1350  
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aaaaagcagc ccttttgctt ttttggtttt ggaccaggtg ttggctgtgg 1450  
tgttattaga aatgtcttaa ccacagcaag aaggaggtgg tggctcata 1500  
ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550  
tttaaagatg cttgggccag ggggggtggc tgatgccat aatcccagtg 1600  
ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
 gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttggggaggct 1750  
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
 ctgaaaaga 1809

<210> 72  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile  
 1 5 10 15  
 Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly  
 20 25 30  
 Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
 35 40 45  
 Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
 50 55 60  
 Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
 65 70 75  
 Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
 80 85 90  
 Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
 95 100 105  
 Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
 110 115 120  
 Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
 125 130 135  
 Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
 140 145 150  
 Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
 155 160 165  
 Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
 170 175 180  
 Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
 185 190 195  
 Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
 200 205 210  
 Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
 215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 74  
 tggtaaactg gcccaaaactc gg 22

<210> 75  
 <211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcac cgcctccttg ctcaggattt ggagagcttg caccaccaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50  
ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100  
tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagg 200  
caccgacggc cccccggcca cccccgccta ctgggacggc gagaaggagg 250  
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350  
ctgggaccgg cagccgcccg ggggtcccga cgaccgcgcg gaccgcctgc 400  
tggaacctta cgcgtcgggc gagcgcgcgc cctacgggce cctttttctg 450  
cgcgaccgcg tggctgtggg cgcgcatgcc tttagcgcgc gtgacttctc 500  
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550  
acctgcacca ccattactgt ggcccgacg aacgcgcgt cttccacctg 600  
acggtcgccg aacccaacgc ggagccgccc ccccggggct ctccgggcaa 650  
cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700  
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccactttctc 750  
cagcagctgg gctacgtgct ggccacgctg ctgctcttca tcctgctact 800  
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tggctgagga caggggaggg agtgaagttg gtttgggggtg gcctgtgttg 1900  
ccactctcag caccacacat ttgcatctgc tgggtggacct gccaccatca 1950  
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu  
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp  
20 25 30  
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens

<400> 78

cgccggaggc agcggcgggc tggcgcagcg gcgacatggc cgttgtctca 50  
gaggacgact ttcagcacag ttcaaactcc acctacggaa ccacaagcag 100  
cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
cactgccaag gagtactgga tgttcaaact cgcgaactcc tccagcccag 300  
ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350  
taccttgccg ttgcctccac cgtgcctcc atgctgtgcc tgggtggcaa 400  
cttctgtctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450  
tgacgggcat cctggccatc ttcattggtga taactgcaact ggtgaagggtg 500  
gacacttctt cctggaccgc tgggtttttt gcggtcacca ttgtctgcat 550  
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gccatgggcg ggacggtcag cgccgtggcc tcattggtgg acttggctgc 700  
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gattcattga ttccacaca cccctctcc gcccctcct gaagaagacg 950  
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cactgtggac caccaagttt ttcattcccc tcaactacct cctcctgtac 1100  
aactttgctg acctatgtgg ccggcagctc accgcctgga tccaggtgcc 1150  
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tcatccccct cttcgtgtc tgtaactacc agcccccggt ccacctgaag 1250  
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tatgtgtgct tgggcttaac actgggctca gcctgctcta cctcctggt 1450



gcacctcatc tagaagggag gacacaagga cattggtgct tcagagcctt 1500  
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taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600  
cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650  
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acaaatcagg ggtactccct tcacagctga tggttaacat tccaccttct 1750  
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gccagtgcc aaaccagcc atgggctctt tgcaacctcc cagctgcgct 1850  
cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900  
gaaggggtct ccctggaatg gaagtccctt ggcatggtca gtcctcaggc 1950  
ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000  
ccactaacca gactggaaaa ccagaaaaga tgggccttcc atgaatgctt 2050  
cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100  
ggcctggggt ttcaaaaaaa gagggatcct catgacctgg tgggtctatgg 2150  
cctgggtcaa gatgagggtc tttcagtgtt cctgtttaca acatgtcaaa 2200  
gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79  
<211> 475  
<212> PRT  
<213> Homo sapiens

<400> 79  
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser  
1 5 10 15  
Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala  
20 25 30  
Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg  
35 40 45  
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
50 55 60  
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
65 70 75  
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
80 85 90  
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395	400	405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser	Ser
	410	415	420
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu	Leu
	425	430	435
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr	Gly
	440	445	450
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly	Ser
	455	460	465
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile	
	470	475	

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 80  
 ttttgcggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844

<212> DNA  
<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50  
ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100  
tcctcgtcct cgtcccatc ctctcagcc tggcggcctc ccaggactgg 150  
aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tggtgacctg ggggctcaat cggaccctga 250  
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300  
gccaaagtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350  
taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400  
ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450  
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500  
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
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aagggccact cggccgaaga catctaccag atggctctca accaggccct 650  
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700  
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 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu  
 1 5 10 15  
 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln  
 20 25 30  
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro	Glu
170		175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu	Lys
185		190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200		205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215		220	225
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230		235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245		250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260		265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275		280	285
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290		295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305		310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320		325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335		340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350		355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365		370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380		385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395		400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410		415	420
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425		430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440		445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu

	455		460		465
Lys Asp Asp Trp	Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly			
	470	475			480
Glu His Thr Ala	Tyr Pro His Gly Trp	Val Glu Thr Ala Val Lys			
	485	490			495
Ser Ala Leu Arg	Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly Pro			
	500	505			510
Ala Ser Asp Thr	Ala Ser Pro Glu Gly	His Ala Ser Asp Met Glu			
	515	520			525
Gly Gln Gly His	Val His Gly Val Ala	Ser Ser Pro Ser His Asp			
	530	535			540
Leu Ala Lys Glu	Glu Gly Ser His Pro	Pro Val Gln Gly Gln Leu			
	545	550			555
Ser Leu Gln Asn	Thr Thr His Thr Arg	Thr Ser His			
	560	565			

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 ctctggggccg gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100  
 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150  
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
 cccctcgcga gggctcgaat ttctgtctgc tgttcacaaa gatgcttttt 250  
 atctttaact ttttgttttc cccacttccg accccggcgt tgatctgcat 300  
 cctgacattt ggagctgcca tcttcttggtg gctgatcacc agacctcaac 350  
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgagggg 400  
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450  
 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgctg 500  
 tgtctgacaa tgggccctgc ttgggatata gaaaacaaa ccagccctac 550  
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600  
 ctgtctcttg cataaagggt ataaatcatc accagaccag tttgtcggca 650  
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 <212> PRT  
 <213> Homo sapiens

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Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	
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Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	
				65					70					75	
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	
				80					85					90	
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	
				95					100					105	
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	
				110					115					120	
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	
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Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	
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Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	
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Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	
				170					175					180	
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	
				185					190					195	
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	
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Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	
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Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	
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Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	
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Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	
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Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	
				275					280					285	
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	
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Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	
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His	Gln	Asn	Ile	Val	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val
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Glu	His	Ala	Tyr	Glu	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr
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Leu	Pro	Leu	Ala	His	Met	Phe	Glu	Arg	Ile	Val	Gln	Ala	Val	Val
				365					370					375
Tyr	Ser	Cys	Gly	Ala	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg
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Ala	Val	Pro	Arg	Leu	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn
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Glu	Ala	Lys	Thr	Pro	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val
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Ser	Ser	Lys	Phe	Lys	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp
				440					445					450
Ser	Phe	Trp	Asp	Lys	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu
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Gly	Gly	Arg	Val	Arg	Val	Ile	Val	Thr	Gly	Ala	Ala	Pro	Met	Ser
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Thr	Ser	Val	Met	Thr	Phe	Phe	Arg	Ala	Ala	Met	Gly	Cys	Gln	Val
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Tyr	Glu	Ala	Tyr	Gly	Gln	Thr	Glu	Cys	Thr	Gly	Gly	Cys	Thr	Phe
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Thr	Leu	Pro	Gly	Asp	Trp	Thr	Ser	Gly	His	Val	Gly	Val	Pro	Leu
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Ala	Cys	Asn	Tyr	Val	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr
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Phe	Thr	Val	Asn	Asn	Glu	Gly	Glu	Val	Cys	Ile	Lys	Gly	Thr	Asn
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Val	Phe	Lys	Gly	Tyr	Leu	Lys	Asp	Pro	Glu	Lys	Thr	Gln	Glu	Ala
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Leu	Pro	Asn	Gly	Thr	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile
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Phe	Lys	Leu	Ala	Gln	Gly	Glu	Tyr	Ile	Ala	Pro	Glu	Lys	Ile	Glu
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Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
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Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
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Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
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Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
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Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
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His Ile Gln Asp

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 <212> DNA  
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 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105  
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
 110 115 120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
 125 130 135

Leu Asn Gln Ala	Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro	His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro	Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His	Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln	Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly	Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro	Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val	Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr	Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly	Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe	Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val	Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu	Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr	Val Phe Ile Asp Gly Tyr	Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala	Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys	Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr	Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu	Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser	Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
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 <211> 307  
 <212> PRT  
 <213> Homo sapiens

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                   20                  25                  30  
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
                   35                  40                  45  
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
                   50                  55                  60  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
                   65                  70                  75  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
                   80                  85                  90  
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
                   95                  100                  105  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
                   110                  115                  120  
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
                   125                  130                  135  
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
                   140                  145                  150  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
                   155                  160                  165  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
                   170                  175                  180  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
                   185                  190                  195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
                   200                  205                  210  
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
                   215                  220                  225  
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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Asn Ala Thr Gly	Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu		
	245	250	255		
Tyr Val Ala Thr	Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly		
	260	265	270		
His Ser His Lys	Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg		
	275	280	285		
Leu Glu Val Ala	Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile		
	290	295	300		
Leu Ser Val Gly	His Gln His				
	305				

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 <213> Artificial

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 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 97  
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<210> 98  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-50  
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 <211> 1429

<212> DNA  
<213> Homo sapiens

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ccgccccctcg tgctggccgc cctggtggcc tgcacatcg tcttgggctt 200  
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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr
				245					250					255
Asn	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu
				260					265					270
Pro	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val
				275					280					285
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro
				290					295					300
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met
				305					310					315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu
				320					325					330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu
				335					340					345
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser
				350					355					360
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile
				365					370					375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu
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Leu	Asp	Gln	Arg	Glu	Lys	Arg	Asn	His	Thr	Leu				
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<210> 101  
 <211> 3671  
 <212> DNA  
 <213> Homo sapiens

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	170	175	180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	185	190	195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly				

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Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500	505	510	
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515	520	525	
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530	535	540	
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545	550	555	
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560	565	570	
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575	580	585	
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590	595	600	
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605	610	615	
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620	625	630	
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635	640	645	
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650	655	660	
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665	670	675	
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680	685	690	
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695	700	705	
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710	715	720	
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725	730	735	
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740	745	750	
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755	760	765	
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770	775	780	
Thr Pro Phe Ser Gly	Pro Pro Thr Ser Gln	Ala Asp Leu Asp Tyr	

785										790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met		Gln	Glu	Glu	Phe	Arg	Gly				
				800						805					810				
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly		Pro	Leu	Thr	Val	Ala	Ala				
				815						820					825				
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala		Ala	Met	Val	Thr	Ala	Leu				
				830						835					840				
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu		Leu	His	Ala	Glu	Arg	Ile				
				845						850					855				
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu		Gln	Ser	Phe	Leu	Leu	Leu				
				860						865					870				
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val		Thr	Thr	Pro	Gly	Pro	Phe				
				875						880					885				
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala		Trp	Ala	Leu	Met	Ala	Thr				
				890						895					900				
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln		Pro	Val	Phe	Pro	Ala	Ile				
				905						910					915				
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe		Pro	Glu	Gly	His	Gly	Ser				
				920						925					930				
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val		Gly	Ala	Asn	Thr	Phe	Ala				
				935						940					945				
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys		Pro	Leu	Leu	Leu	Leu	Trp				
				950						955					960				
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu		Arg	Lys	Arg	Gln	Gln	Pro				
				965						970					975				
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val		Arg	Pro	Glu	Glu	Glu	Glu				
				980						985					990				
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg		Asp	Ala	Pro	Gln	His	Phe				
				995						1000					1005				
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu		Lys	Tyr	Leu	Phe	Ile	Leu				
				1010						1015					1020				
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu		Ala	Ala	Ser	Ile	Leu	Arg				
				1025						1030					1035				
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe		Ala	Pro	Lys	Phe	Ile	Phe				
				1040						1045					1050				
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser		Val	Gly	Leu	Leu	Leu	Gly				
				1055						1060					1065				
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly		Ala	Val	Ser	Ser	Trp	Phe				
				1070						1075					1080				

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
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gcagttccct gtgtctctgg tggtttgcc aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggc 150  
ttcaaggagt taaagttact taaactgtgc agtatctcat cacaatttgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350  
taaatacaac agaactgggt cccagtgtgt gaccaaccac acgtgtgtgc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450  
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550  
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600  
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcacccctc atatctcgga tgattctaaa 750  
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagccca gcgggaacct gagggccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100  
ggcagtcttg ggcccgaaca cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc 1200  
gaggaagagc catcgacgac cctggctgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300  
 agccttctga ggggggatggg ctcgagagagg agggctcttct atctagactc 1350  
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
 catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450  
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 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
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 cgtgtgtgat tggttcatgc atgtaggctct cttacaatg atgggtgggccc 1650  
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys	1	5	10	15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu	20	25	30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr	35	40	45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser	50	55	60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu	65	70	75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His	80	85	90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165	



Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile		170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys		185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys		200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val		215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro		230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu		245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser		260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys		275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys		290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser		305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu		320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp		335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro		350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr		365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser		380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly		395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro		410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly		425	430	435
Leu	Tyr	Val	Gln	Met	Glu	Asn										440		

<210> 105

<211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-21  
 <223> Synthetic construct  
  
 <400> 105  
 cgctgctgct gttgctcctg g 21  
  
 <210> 106  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 106  
 cagtgtgccca ggactttg 18  
  
 <210> 107  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 107  
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 <210> 108  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 108  
 ctccctccgag tctgtgtgct cctgc 25  
  
 <210> 109  
 <211> 51  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
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tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150  
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttcctgctg cgagcccgt ggggtgtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgactggc ctggtgtgctc tgggcgccc cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccatga cccacgcaa cgacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500  
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctgg 550  
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600  
ccaaggtccg agtctgggac ccggacgtct gcaacagctc ctggaagggc 650  
cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700  
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cccacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850  
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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
gccgctccag gcctggaatg ttccgtggct gggcccacg ggaagcctga 1000  
tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
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aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
 275 280

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 112  
 gacgtctgca acagctcctg gaag 24

<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 113  
 cgagaaggaa acgaggccgt gag 23

<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-44  
 <223> Synthetic construct.

<400> 114  
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<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
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 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
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ggtcatcgtg acgggcgcca acacaggcat cggaagcag accgccttgg 250  
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 gtccctctctg agccttgggt tcttcagcag tgagatgctc agaataactg 1550  
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<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116

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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	
His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccc 150  
 agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400  
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450  
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500  
 agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600  
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700



agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 cccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000  
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450  
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 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctgggtg agtcctgtgg ctttccagag 1700  
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800  
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850  
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtggg 1900  
 ggctgagag ggaagtctct ggagttcaga tactctctgt tgggaacagg 1950  
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000  
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
 tagcctgact cccagaactt taagaacttc tccccactgc cttctgctgc 2100  
 agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	
1				5					10					15	
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	
				20					25					30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	
				35					40					45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	
				50					55					60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	
				65					70					75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	
				80					85					90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	
				95					100					105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	
				110					115					120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	
				125					130					135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	
				140					145					150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	
				155					160					165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	
				170					175					180	
Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly	
				185					190					195	
Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu	
				200					205					210	
Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser	
				215					220					225	
Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala	
				230					235					240	

Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser	Val Glu Ala Gly Gly	Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser	Val Pro Val Val Arg	Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His	Arg Ser Gly Glu Gly	Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro	Val Leu Val Gly Asp	Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu	Tyr Gly Gln Glu Phe	Arg Arg Pro Cys Ser Ser			

Ser Pro Glu Asp

<210> 119  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 119  
cgggacagga gacccagaaa ggg 23

<210> 120  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 120  
ggccaagtga tccaaggcat cttc 24

<210> 121  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 121  
ctgcgggacc tgactagatt ctacgacaag gtactttcctt tgcattgggg 49

<210> 122  
<211> 1778  
<212> DNA  
<213> Homo sapiens

<400> 122  
gagataggga gtctgggttt aagttcctgc tccatctcag gagccctgc 50  
tcccaccctt aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
 gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
 ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400  
 gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
 ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550  
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
 aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
 cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750  
 gcacaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
 atcgacaagg agcgtttcag tgtgcaggat gtcactctacg tgcggggctg 850  
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
 gcatectcct gggcatectg cttccccagt tcctgggggt gctgctgacg 950  
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000  
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050  
 cgggatgctg cttgtgttac cccaattagg gccagcctg ccatggcagc 1100  
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
 ggacagggt gcggccctc tgccacact cagtactgac caaagccagg 1200  
 gctgtgtgtg cctgtgtgta ggtccacgg cctctgcctc ccagggagc 1250  
 agagcctggg cctcccctaa gaggtttcc ccgaggcagc tctggaatct 1300  
 gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350  
 ctacagggga gggagagcct gaggtctgc tcagggccca ttcatctct 1400  
 ggcagtgcct tggcggtggg attcaaggca gttttgtagc acctgtaatt 1450  
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500  
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550  
 ctcttctcag cctcccagg gccttgagcc ctcttgcaag ggcggtgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgттаatcaa acaataaaaa 1750  
 catgttttgt ttgttttta aaaaaaaa 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
 1 5 10 15  
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
 20 25 30  
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
 35 40 45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
 170 175 180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
 185 190 195  
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
 200 205 210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
 215 220 225  
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr			
	245	250		255	
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp			
	260	265		270	
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly			
	275	280		285	
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150  
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtctgaagc acatcatctg gctgaaggct atcacagcta 350  
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450  
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccacccgcc tggtcctcag tgactgtgcc 550  
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600  
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700  
ggcatgtatg cagacctcct gcagctgggtg aaggtgcccc tttccctcag 750  
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800  
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850  
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900  
caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950  
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aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa 1150  
ctgatcgtgc tggaaagtgt tccctccagt gaagccctcc gccctttgtt 1200  
caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400  
gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450



gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500  
 gaaacccagc tctcctgtct cccagtgaag acttggtggtg cagccatcag 1550  
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128  
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala  
 1 5 10 15  
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
 20 25 30  
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
 35 40 45  
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
 50 55 60  
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
 65 70 75  
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
 80 85 90  
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
 95 100 105  
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
 110 115 120  
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
 125 130 135  
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
 140 145 150  
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
 155 160 165  
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
 170 175 180  
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
 185 190 195  
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
 200 205 210  
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
 215 220 225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro Val Ser Gln																	

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcgggtttt ggtgtgtctc tgtgaccatg 50  
gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccc aaag 100  
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
ttttttgcc a tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400  
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450  
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<210> 130  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
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 20 25 30  
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 35 40 45  
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 50 55 60  
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
 65 70 75  
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
 80 85 90  
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
 95 100 105

Tyr Ser Ser Ala	Phe Thr Asn Arg Ile	Phe Phe Ala Met Val	Asp
	110	115	120
Phe Asp Glu Gly	Ser Asp Val Phe Gln	Met Leu Asn Met Asn	Ser
	125	130	135
Ala Pro Thr Phe	Ile Asn Phe Pro Ala	Lys Gly Lys Pro Lys	Arg
	140	145	150
Gly Asp Thr Tyr	Glu Leu Gln Val Arg	Gly Phe Ser Ala Glu	Gln
	155	160	165
Ile Ala Arg Trp	Ile Ala Asp Arg Thr	Asp Val Asn Ile Arg	Val
	170	175	180
Ile Arg Pro Pro	Asn Tyr Ala Gly Pro	Leu Met Leu Gly Leu	Leu
	185	190	195
Leu Ala Val Ile	Gly Gly Leu Val Tyr	Leu Arg Arg Ser Asn	Met
	200	205	210
Glu Phe Leu Phe	Asn Lys Thr Gly Trp	Ala Phe Ala Ala Leu	Cys
	215	220	225
Phe Val Leu Ala	Met Thr Ser Gly Gln	Met Trp Asn His Ile	Arg
	230	235	240
Gly Pro Pro Tyr	Ala His Lys Asn Pro	His Thr Gly His Val	Asn
	245	250	255
Tyr Ile His Gly	Ser Ser Gln Ala Gln	Phe Val Ala Glu Thr	His
	260	265	270
Ile Val Leu Leu	Phe Asn Gly Gly Val	Thr Leu Gly Met Val	Leu
	275	280	285
Leu Cys Glu Ala	Ala Thr Ser Asp Met	Asp Ile Gly Lys Arg	Lys
	290	295	300
Ile Met Cys Val	Ala Gly Ile Gly Leu	Val Val Leu Phe Phe	Ser
	305	310	315
Trp Met Leu Ser	Ile Phe Arg Ser Lys	Tyr His Gly Tyr Pro	Tyr
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Ser Phe Leu Met	Ser		
	335		

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250  
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 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
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<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
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 20 25 30  
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
 35 40 45  
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
 50 55 60  
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly		80	85	90
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu		95	100	105
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly		110	115	120
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His		125	130	135
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala		140	145	150
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg		155	160	165
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr		170	175	180
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr		185	190	195
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr		200	205	210
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His		215	220	225
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys		230	235	240
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr		245	250	255
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys		260	265	270
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu		275	280	285
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu		290	295	300
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly		305	310	315
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr		320	325	330
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile		335	340	345
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile		350	355	360
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn				



365										370					375				
Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Ser	Glu	Thr	Phe	Lys				
				380					385						390				
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser					
				395					400					405					
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg					
				410					415					420					
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile					
				425					430					435					
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr					
				440					445					450					
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln					
				455					460					465					
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val					
				470					475					480					
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile					
				485					490					495					
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln					
				500					505					510					
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln					
				515					520					525					
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val									
				530					535										

<210> 133  
 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
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 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
 catcacccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350  
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 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
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 cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350  
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
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Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala
				65					70					75
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile
				80					85					90
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr
				95					100					105
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala
				110					115					120
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro
				125					130					135
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro
				140					145					150
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr
				155					160					165
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile
				170					175					180
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr
				185					190					195
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg
				200					205					210
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser
				215					220					225
Leu	Thr	Gly	Tyr	Val										
				230										

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 aagtcatcgc tcccgctggc tcagaaccat ggctgtgcca gccggcaccc 150  
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 cgccatcgtg tccctgagcg agaccgcga atgtgggtccc cctgcacct 250  
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 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
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 aggtaatatg tgtaccagta gagaagcctg aggaattttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
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 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
 65 70 75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
 80 85 90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
 95 100 105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
 110 115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

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 agaactgcga ctcagcccgg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30

Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45

Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60

Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75

Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90

Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105

Cys	Arg	Ser	Val	Ser
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<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagttc ctctgcgct cgcagggca catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcg tggggatccc tgctcttcgc 200  
 tctcttctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250  
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 caccaggctg ccaacaccag ccacgacctg gtcagcgcc acgggctgga 500  
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
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 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
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 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850  
 gggaaggatga gtggagaggg gcacctgccc cccgccctcc ccattccccta 1900  
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 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
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 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val  
 20 25 30  
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140										145					150				
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu					
				155					160					165					
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val					
				170					175					180					
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala					
				185					190					195					
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu					
				200					205					210					
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg					
				215					220					225					
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile					
				230					235					240					
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro					
				245					250					255					
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln					
				260					265					270					
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro					
				275					280					285					
Leu	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Val	Phe	Phe	Pro	Ser	Leu	Asp					
				290					295					300					
Pro	Val	Pro	Asp	Ser	Pro	Asn	Phe	Glu	Val	Ile									
				305					310										

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc ctttctgcc ctcccttccct gccacccgct gcttccctggc 150  
 ccttctccga ccccgtcta gcagcagacc tctgggggtc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtccctttt cgtctccctt cctcccgact 250  
 ccgctcccg accagcgcc tgaccctggg gaaaggatgg ttcccgaggt 300  
 gagggctctc tctccttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccattgggaag 400  
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450



gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650  
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700  
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
ccccgaacca ggctgccag caccctccc actgccagac tcctgctgcc 800  
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
tgggagaaag agaggcccgg gcacccagc cccactggc ctcagcggcc 950  
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000  
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100  
tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150  
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200  
agtggctggg aagtgtgca agatttggcc agaggacaaa gcagaccctg 1250  
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400  
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
cca'cacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500  
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550  
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
gatatgagct gtataattgt tggtattata tattaataaa taagaagttg 1700  
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens  
<400> 142

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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290										295					300				
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro					
				305					310					315					
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg					
				320					325					330					
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser					
				335					340					345					
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala					
				350					355					360					
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu					
				365					370					375					
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His					
				380					385					390					
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala					
				395					400					405					
Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro					
				410					415					420					
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala					
				425					430					435					
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys					
				440					445					450					

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
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 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400  
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtcgggaccg agataccatg ccaggactct ccggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
     1                    5                    10                    15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
                     20                    25                    30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
                     35                    40                    45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
                     50                    55                    60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
                     65                    70                    75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
                     80                    85                    90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 ttgaggggaa gaggtgact gtacgttctt tctactctgg caccactctc 100  
 caggctgccca tggggcccag caccctctc ctcatottgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
tggaggccct gggaccaaag gcaaggaag aaggaatgag aagtacgata 500  
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600  
gcaaacagag aagatctaçg tgttagatgg gacacagaat gacacagcct 650  
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gcttcccagag tccgggtgcc ctccccctgg gtaggcacag ggcagctggg 750  
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900  
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
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accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
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tcctttgatg ccagcggcac cctgaccctt gaacgggcag cactccctta 1200  
ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
catctttctc actcccatac atttatatta tatccccact aaatttcttg 1400  
ttcctcattc ttcaaagtgt ggccagttgt ggctcaaçtc ctctatatatt 1450  
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ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
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cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650  
agcagtgttc ttcccctcag agtgacttgg ggaggggagaa ataggaggag 1700  
acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750  
aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
			20						25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35						40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
			50						55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
			65						70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
			80						85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
			95						100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
			110						115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
			125						130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
			140						145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
			155						160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
			170						175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
			185						190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
			200						205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
			215						220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
			230						235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
			245						250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	260	265	270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	275	280	285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	290	295	300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	320	325	330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	335	340	345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	350	355	360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	365	370	375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	380	385	390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	395	400	405

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50  
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100  
 gttctctctt tctctctaatt ccatccgtca cctctctctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttctctgc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag' agacatgcat ggctgtttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850  
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950  
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100  
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 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaaatcc ccgttttate agcgtcttcc ccaggacccc acctacaaaa 1400  
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
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 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctccc aggggtgaaa tgtaggatga atcacatccc 1700  
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 cattacattt agtttgcctt cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950



tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgctgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccggtggc ggtggcgggc gcggttgccg aggccttcctt 50  
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctggggc 150  
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cggtgggcggc ggggccgcgg ggcaggtgga 250  
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350  
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
cgctcgggcc ctcgccgacc acccctccgg cggcggaacg cacttcgacc 500  
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550  
tggcccgggc ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600  
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650  
ctccccaccc cacctgccac cgaggccccc tcttcgctc ctccagagta 700  
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750  
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800  
gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850  
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaacaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaaaca aggaggatga 1000  
gggtcataga tttacaaaat attttatata cttttattct cttactttat 1050  
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100  
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150  
atctcatggg aaaaaattat tgaagaataa atctgctttc tggaagggct 1200  
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250  
atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300  
taatcaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350  
ggtaccctaa tttatttaac tagtggtgag tagactgggt ttactctatt 1400  
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
aactattatg ttatttgag gtaatttaac ctagtggaat aatgtactgt 1500  
tatctaagca tttgccttg actgcactga aagtaattat tctttgacct 1550  
tatgtgaggc acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600  
acagtattaa ataataaaaa aaataatgac aggttatact cagtgtgtaacc 1650  
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ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900  
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050  
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 ctactaaaaa tacaacaaaa ttagctgggc gtggtggcac acacctgtag 2150  
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
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 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153  
 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys  
 1 5 10 15  
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn  
 20 25 30  
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro  
 35 40 45  
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala  
 50 55 60  
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala  
 65 70 75  
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro  
 80 85 90  
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr  
 95 100 105  
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala  
 110 115 120  
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro  
 125 130 135  
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val  
 140 145 150  
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro  
 155 160 165  
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

	170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn			
	185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr			
	200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys			
	215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu			
	230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro			
	245	250	255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
 aactgctctg tggttggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgagcag ttagacacgtg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggctttt ggtctcggtg cccagggccc aggcctgtg gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cgggtggcctc 150  
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgta ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcc aatcttcac tcagctggag 400  
 ttctggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600  
 gggctcctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
     1                    5                    10                    15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
                     20                    25                    30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
                     35                    40                    45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
                     50                    55                    60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
                     65                    70                    75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
                     80                    85                    90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50  
 gctgctgctg ccctgctct gggggaggga gagggcgga ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
 gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacc 200  
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250  
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgtcctcg gtgctcacc tcatcccaca 650  
 gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
 tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900  
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950



ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050  
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100  
 tggagccaca gccctgggtc tcctgtcctt ctgcgtcatc ttcgtttag 1150  
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250  
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
 cttctgcccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttcacaga tggatgaagc ttgggactcg cggggacagg agggcactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgcctccct tttattttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

	110		115		120
Met Glu Lys Gly	Ser Ile Lys Trp Asn	Tyr Lys His His Arg	Leu		
	125	130	135		
Ser Val Asn Val	Thr Ala Leu Thr His	Arg Pro Asn Ile Leu	Ile		
	140	145	150		
Pro Gly Thr Leu	Glu Ser Gly Cys Pro	Gln Asn Leu Thr Cys	Ser		
	155	160	165		
Val Pro Trp Ala	Cys Glu Gln Gly Thr	Pro Pro Met Ile Ser	Trp		
	170	175	180		
Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg	Ser		
	185	190	195		
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr	Ser		
	200	205	210		
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr	Asn		
	215	220	225		
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu	Thr		
	230	235	240		
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu	Gly		
	245	250	255		
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg	Leu		
	260	265	270		
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg	Leu		
	275	280	285		
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro	Ser		
	290	295	300		
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp	Ala		
	305	310	315		
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln	Gln		
	320	325	330		
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly	Val		
	335	340	345		
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val	Phe		
	350	355	360		
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg	Lys		
	365	370	375		
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile	Glu		
	380	385	390		
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu	Thr		
	395	400	405		

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggctcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200  
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250  
 gaggagggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550  
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650  
 gctccacccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	Arg				
				35					40						45				
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly	Gly				
				50					55						60				
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile	Ile				
				65					70						75				
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	Tyr				
				80					85						90				
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	Pro				
				95					100						105				
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	Gly				
				110					115						120				
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	Thr				
				125					130						135				
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	Lys				
				140					145						150				
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	Ser				
				155					160						165				
Cys	Val	Pro	Glu	His															
				170															

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag,accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cgggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggt gaggtggctg cgggactgga agtcatcggg 50  
 cagagggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150  
 gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200  
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250  
 cgacgtcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300  
 ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350  
 ctgtgagcag acccgagacag cactgagtc cttccccac cccggcttca 400  
 acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
 atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500  
 ctcacgtgt gtactgctg gcaccagctg cctcatttcc ggctggggca 550  
 gcacgtccag ccccagtta cgctgcctc acaccttgcg atgcgccaac 600  
 atcaccatca ttgagacca gaagtgtgag aacgcctacc ccggcaacat 650  
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
 gccagggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
 attatctcct ggggccagga tccgtgtgag atcacccgaa agcctggtgt 800  
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850  
 acaattagac tggaccacc caccacagcc catcacctc catttccact 900  
 tgggtgtttg ttctgttca ctctgttaat aagaaacct aagccaagac 950  
 cctctacgaa cattctttg gcctcctgga ctacaggaga tgctgtcact 1000  
 taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050  
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100  
 tgtatcccca gcccgaaga cagtcctgg ccatatatca aggtttcaat 1150  
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaa 1204

<210> 170  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
 1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc gggtg 25

<210> 176  
<211> 18  
<212> DNA



<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgcaaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttagattg aactttatgc 450  
 tgtgacaaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850  
 ttgcaaacctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe	1	5	10	15
Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150	

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu  
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys  
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu  
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser  
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu  
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgtttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-27  
<223> Synthetic construct.

<400> 185  
gcatcctgat atgacttgct acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 186  
tacaagaggg aagaggagtt gcac 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-52  
<223> Synthetic construct.

<400> 187  
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
cc 52

<210> 188  
<211> 573  
<212> DNA  
<213> Homo sapiens

<400> 188  
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50  
ctctttggag ctgtgactca gaaaacaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aacctatggat 150  
 atactttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200  
 aacgccaggc atggtggctc ggcctgtaa tcccagttct ttgggaagcc 250  
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350  
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550  
 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
gactttggaa gtgaccacc atggggctca gcatcttttt gtcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgcttggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
tgctcaacc tctccatcgt ctccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tgggtgtgtc aggcggcgtc ccggggcagg 700  
atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtcctt 750  
caaggctctg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttgttg gcctgggaac ttcttgaac tttaactcct 1000  
 gccagccctt ctaagaccca cgagcgggt gagagaagtg tgcaatagtc 1050  
 tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val	Ser Trp Gly Ser Val	Gly Pro Cys Gly Gln Asp			
	215	220		225	
Gly Ile Pro Gly	Val Tyr Thr Tyr Ile	Cys Lys Tyr Val Asp Trp			
	230	235		240	
Ile Arg Met Ile	Met Arg Asn Asn				
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe	1	5	10	15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn	20	25	30	
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu	35	40	45	
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp	50	55	60	
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met	65	70	75	
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys	80	85	90	
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr	95	100	105	
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu	110	115	120	
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro	125	130	135	
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<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	170	175	180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Ile	Ser	Arg		185	190	195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	200	205	210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	215	220	225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	230	235	240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	245	250	255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	260	265	270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	275	280	285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	290	295	300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	305	310	315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	320	325	330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	335	340	345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	350	355	360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	365	370	375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	380	385	390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	395	400	405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	410	415	420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	425	430	435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	440	445	450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser			

455					460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn
				605					610					615
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala Lys			



1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly 1055 1060 1065		
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala 1070 1075 1080		
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly 1085 1090 1095		
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu 1100 1105 1110		
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln 1115 1120 1125		
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu 1130 1135 1140		
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu 1145 1150 1155		
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu 1160 1165 1170		
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln 1175 1180 1185		
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190 1195 1200		
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205 1210 1215		
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220 1225 1230		
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235 1240 1245		
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250 1255 1260		
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265 1270 1275		
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280 1285 1290		
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295 1300 1305		
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310 1315 1320		
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325 1330 1335		

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
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 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
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 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
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 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
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 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
 1415 1420 1425  
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
 1430 1435 1440  
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
 1445 1450 1455  
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
 1460 1465 1470  
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
 1475 1480 1485  
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
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 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
 1505 1510 1515  
 Glu Cys Gly Cys Leu Ala Cys Ser  
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<210> 199  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 199  
 atggagattc ctgccaactt gccg 24

<210> 200  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>

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<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcacgc tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccgt ttctcccaa tattccttct caaacttgga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr
1				5					10					15
Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115					120
Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys	Lys	His	Cys	Glu	Gly
				125					130					135
Arg	Asp	Leu	Ser	Glu	Trp	Lys	Lys	Gly	Cys	Glu	Val	Ser		
				140					145					

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 204

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<210> 205  
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<222> 1-24

<223> Synthetic construct.

<400> 205  
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<210> 206  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 206  
 ccagtcggac aggtctctcc cctc 24

<210> 207  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-24  
 <223> Synthetic construct.

<400> 207  
 tcagtgacca aggctgagca ggcg 24

<210> 208  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-47  
 <223> Synthetic construct.

<400> 208  
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<210> 209  
 <211> 1648  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
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 tattaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
 gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
 gaggaatata ccacagggcat ggcagactgc atcttagtca acagccagtt 350  
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcagttggt 450  
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
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 ccctagtaca gctgctgga agattgacat cccaagattg ggagaggggt 600  
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 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
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 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
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 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
 gagcctgacc cgggtgcactt ctgagaagca atagaaaagt tcatccgtga 950  
 accttctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
 aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050  
 aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100  
 ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150  
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
 ctttctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300  
 tgtcattcca tgttcagcag agtattttta ttatattttc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gttcatagt 1450  
 ataagagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcaatgcat ctgttaggga atttttgttt gtccctgtct tgccctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaagggt gtttatcata aaaaaaaaaa aaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT  
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
tttgcattgag ttccctggta atttgcattg gagatatggg cctgtggtct 250
ccttctgggt tggcaggcgc ctccgtggta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
accacattgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
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tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
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gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

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ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
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 tgaccgattt attattccta gagagaccct cgtccctttat gcccttggtg 1150  
 tgggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200  
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 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu

140										145					150				
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser					
				155					160					165					
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val					
				170					175					180					
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln					
				185					190					195					
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu					
				200					205					210					
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu					
				215					220					225					
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys					
				230					235					240					
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser					
				245					250					255					
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser					
				260					265					270					
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys					
				275					280					285					
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys					
				290					295					300					
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val					
				305					310					315					
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu					
				320					325					330					
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln					
				335					340					345					
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg					
				350					355					360					
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro					
				365					370					375					
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp					
				380					385					390					
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly					
				395					400					405					
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr					
				410					415					420					
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val					
				425					430					435					

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
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<210> 213  
<211> 759  
<212> DNA  
<213> Homo sapiens

<400> 213  
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tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750  
aaaaaaaa 759

<210> 214  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 214  
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
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Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	
				50					55					60	
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	
				65					70					75	
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	
				80					85					90	
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	
				95					100					105	
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	
				110					115					120	
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	
				125					130					135	
Lys	Lys	Lys	Pro	Phe											
				140											

.<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
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 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
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 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
 ctaccgctcc cctgagggcc ctgctgatcc gcacccatt cctccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

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Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	
			20						25					30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	
				35					40					45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	
				50					55					60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	
				65					70					75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	
				80					85					90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	
				95					100					105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	
				110					115					120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	
				125					130					135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	
				140					145					150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	
				155					160					165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	
				170					175					180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	
				185					190					195	

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtccctcccg ctcagaggac 150  
cctgagcgtg atgaccacga gggccagccc cggccccggg tgccctcgga 200

gcggggccac atctcaccta agtcccgcgc catggccaat tccactctcc 250  
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 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400  
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 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550  
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 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850  
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<210> 218  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 218  
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Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser  
20 25 30  
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg  
35 40 45  
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
50 55 60  
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
65 70 75  
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
80 85 90  
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
95 100 105  
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
110 115 120  
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
125 130 135  
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
140 145 150  
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
155 160 165  
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
170 175 180  
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
185 190 195  
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200  
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 ccggggcgctg tccgcgggtgc cggccgtgct gctggctctc acgctgccgg 400  
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 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
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 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaa 1950  
 ttcaaataat ccataatctaa atttagtgca atatcttgct tttgtatag 2000  
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tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
			20					25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35					40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
			50					55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 221  
 acggctcacc atgggctccg 20

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 222  
 aggaagagga gcccttgag tccg 24

<210> 223  
 <211> 40

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 223  
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<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
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tatcatcttc ctcacgcgcg gagctttctt ctggttggtg tctctactga 150  
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
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ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500  
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550  
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tcagcattta taatcctggg gctcatgggc acctgggcat tottagctgc 700  
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750  
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850  
tgaaaatccc tttttctggg ggaattgaga aagaaataaa actatgcaga 900  
ta 902

<210> 225  
<211> 257  
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226

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gagccatctg ggggttcttg ggcccaagaa cgtctcgag aaagacgccg 150  
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 caggccctta gtcttgccaa accccagctg gtggcctttc agtgccattg 3400  
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 cgctctagga ccagggtctg gcttctaagt ttccgtccag tcttcaggca 3600  
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 ccttcgtccc acctggtcca cccagatgc tgaggatggg ggagctcagg 3750  
 cggggcctct gctttgggga tgggaatgtg tttttctccc aaacttggtt 3800  
 ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850  
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				



320					325					330				
Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro	Arg	Val	Leu	Ala
				335					340					345
Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly
				350					355					360
Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser
				365					370					375
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg	Ser	Phe
				380					385					390
Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val
				395					400					405
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys
				410					415					420
Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala
				425					430					435
Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe
				440					445					450
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val
				455					460					465
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn
				470					475					480
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly
				485					490					495
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile
				500					505					510
Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile
				515					520					525
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu
				530					535					540
Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr
				545					550					555
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys
				560					565					570
Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met
				575					580					585
Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro
				590					595					600
Asp	Ile	Asn	Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile
				605					610					615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
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Arg	Asp	Lys	Ile	Tyr	Val	Phe									
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<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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ttgggcgctg gagggcctgt cctgaccatg gtcctgcct ggctgtggct 150

gctttgtgtc tccgtcccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc ttatatacctg 250  
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300  
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350  
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 taccagctac aggtcacctt ggagatgcag gatggacatg tcttgtgggg 450  
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20										25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
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Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn
				320					325					330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile
				335					340					345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala
				350					355					360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr
				365					370					375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
				455					460					465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
				470					475					480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
				530					535					540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly

605					610					615				
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp
				620					625					630
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
				635					640					645
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His
				650					655					660
Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser
				665					670					675
Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val
				680					685					690
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr
				695					700					705
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile
				710					715					720
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
				725					730					735
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
				740					745					750
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
				755					760					765
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
				770					775					780
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
				785					790					795
Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val			
				800					805					

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

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<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<221> Artificial Sequence  
<222> full  
<223> Synthetic oligonucleotide probe

<400> 231  
cctgagctgt aaccccactc cagg 24

<210> 232  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 232  
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<210> 233  
<211> 2786  
<212> DNA  
<213> Homo sapiens

<400> 233  
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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250  
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300  
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
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<210> 234  
 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 234  
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                     20                    25                    30  
 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn  
                     35                    40                    45  
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe  
                     50                    55                    60  
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala  
                     65                    70                    75  
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr  
                     80                    85                    90  
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met  
                     95                    100                    105  
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr  
                     110                    115                    120  
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn  
                     125                    130                    135  
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly  
                     140                    145                    150  
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr  
                     155                    160                    165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	
				170					175					180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	
				185					190					195	
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	
				200					205					210	
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	
				215					220					225	
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
				230					235					240	
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	
				245					250					255	
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	
				260					265					270	
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	
				275					280					285	
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	
				290					295					300	
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	
				305					310					315	
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
				320					325					330	
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
				335					340					345	
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	
				350					355					360	
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
				365					370					375	
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
				380					385					390	
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
				395					400					405	
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	
				410					415					420	

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
cccgccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200  
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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
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                     20                    25                    30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
                     35                    40                    45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
                     50                    55                    60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
                     65                    70                    75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
                     80                    85                    90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
                     95                    100                    105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
                     110                    115                    120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
                     125                    130                    135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
                     140                    145                    150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
                     155                    160                    165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
                     170                    175                    180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
                     185                    190                    195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

	200	205	210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe
	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

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<210> 238

<211> 47  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.  
  
 <400> 238  
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 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 239  
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 <212> DNA  
 <213> Artificial  
  
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 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 240  
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 <210> 241  
 <211> 48  
 <212> DNA  
 <213> Artificial  
  
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 <222> 1-48  
 <223> Synthetic construct.  
  
 <400> 241  
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 <210> 242  
 <211> 2436  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 242  
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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	80	85	90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	95	100	105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala			

	365		370		375
Thr Asn Ser Glu	Ser 380	Ser Thr Val Ser	Ser 385	Gly Ala Ser Thr	Ala 390
Thr Asn Ser Glu	Ser 395	Ser Thr Thr Ser	Ser 400	Gly Val Ser Thr	Ala 405
Thr Asn Ser Glu	Ser 410	Ser Thr Thr Ser	Ser 415	Gly Ala Ser Thr	Ala 420
Thr Asn Ser Asp	Ser 425	Ser Thr Thr Ser	Ser 430	Glu Ala Ser Thr	Ala 435
Thr Asn Ser Glu	Ser 440	Ser Thr Val Ser	Ser 445	Gly Ile Ser Thr	Val 450
Thr Asn Ser Glu	Ser 455	Ser Thr Thr Ser	Ser 460	Gly Ala Asn Thr	Ala 465
Thr Asn Ser Gly	Ser 470	Ser Val Thr Ser	Ala 475	Gly Ser Gly Thr	Ala 480
Ala Leu Thr Gly	Met 485	His Thr Thr Ser	His 490	Ser Ala Ser Thr	Ala 495
Val Ser Glu Ala	Lys 500	Pro Gly Gly Ser	Leu 505	Val Pro Trp Glu	Ile 510
Phe Leu Ile Thr	Leu 515	Val Ser Val Val	Ala 520	Ala Val Gly Leu	Phe 525
Ala Gly Leu Phe	Phe 530	Cys Val Arg Asn	Ser 535	Leu Ser Leu Arg	Asn 540
Thr Phe Asn Thr	Ala 545	Val Tyr His Pro	His 550	Gly Leu Asn His	Gly 555
Leu Gly Pro Gly	Pro 560	Gly Gly Asn His	Gly 565	Ala Pro His Arg	Pro 570
Arg Trp Ser Pro	Asn 575	Trp Phe Trp Arg	Arg 580	Pro Val Ser Ser	Ile 585
Ala Met Glu Met	Ser 590	Gly Arg Asn Ser	Gly 595	Pro	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttccccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgaggggtg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaaag 400

gaagcagaga agcttgcca tgggggtcaac aacgtgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
 agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800  
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900  
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950  
 tacacca 957

<210> 248  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 251  
 tgacccatt gagaaggatca ttgaaggat caaccgaggg ctg 43

<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccggggccg gcctggcaag ggggacgagt 50  
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tgaccctgac tcaactccagg tccggaggcg gggggccccg gggcgactcg 150  
ggggcggaacc gcggggcgga gctgccgcc gtgagtcagg ccgagccacc 200  
tgagcccagag ccgcgggaca ccgtcgctcc tgctctccga atgtgcgca 250  
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300  
cctcgccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350  
gccgcctccg acctggggcg tcagcccccg gatcagcctg cctctgggct 400  
ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450  
acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500  
agaggccctc tttgcaactca gtagcaacct cagcttcttg ccaggcgggg 550  
agtaccagga gctgcttttg ggtgcagacg cagagaagaa acagcagtgc 600  
agcttcaagg gcaaggacc acagcgcgac tgtcaaaact acatcaagat 650  
cctcctgccg ctacgggca gtcacctgtt cacctgtggc acagcagcct 700  
tcagcccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750  
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800  
cgaccogaat ttcaagtcca ctgccctggg ggttgatggc gagctctaca 850  
ctggaacagt cagcagcttc caagggaatg acccggccat ctgcgggagc 900  
caaagccttc gccccacca gaccgagagc tccctcaact ggctgcaaga 950  
cccagctttt gtggcctcag cctacattcc tgagagcctg ggagcttgc 1000  
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tttgagttct ttgagaacac cattgtgtcc cgcattgcc gcctctgcaa 1100  
ggcgatgag ggtggagagc ggtgtctaca gcagcgtgg acctccttc 1150  
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gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250  
cacccttttc tatggggtct tcaactccca gtggcacagg ggaactacag 1300  
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gaccacccg gtgccacac cccggcctgg agcgtgcatc accaacagt 1450

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 aacttcctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550  
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 ctctggctac gcaacggggc ccccgtaat gcctcggcct cctgccacgt 2150  
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 tccagtgtg gtcactagag gagggcttcc agcagctggt agccagctac 2250  
 tgcccagagg tgggtggagg cggggtggca gaccaaacag atgaggggtg 2300  
 cagtgtaccc gtcattatca gcacatcgcg tgtgagtga ccagctggtg 2350  
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 tgcccccgcc cccgggtccg ccttggtcgt gagatccgtg actctgtggt 2750  
 gtgagagctg acttcagag gacgctgccc tggcttcagg ggctgtgaat 2800  
 gctcggagag ggtcaactgg acctcccctc cgctctgctc ttcgtggaac 2850  
 acgaccgtgg tgcccggccc ttgggagcct tggagccagc tggcctgctg 2900



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 cagtgtcctt tatgtaaact gagccctttg tttaaaaaac aattccaaat 3050  
 gtgaaactag aatgagaggg aagagatagc atggcatgca gcacacacgg 3100  
 ctgctccagt tcatggcctc ccaggggtgc tggggatgca tccaaagtgg 3150  
 ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200  
 acattatccc gctgccaccg gctgccctgt ctactgcag attcaggacc 3250  
 agcttgggct gcgtgcgttc tgccttgcca gtcagccgag gatgtagtgtg 3300  
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 cctgtatcag gctgtggcca cacgagagga cagcgcgagc tcaggagaga 3450  
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 cctgccttcc tccgttggtg cgtgagaacc cgtgtgcccc tccccaccat 3550  
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 ctggctcctt cccagtgccc cagttcaccc tccatccctc accttccctc 3650  
 actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700  
 gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750  
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253  
 <211> 837  
 <212> PRT  
 <213> Homo sapiens

<400> 253  
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro  
 1 5 10 15  
 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu  
 20 25 30  
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser  
 35 40 45  
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
 50 55 60  
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu  
 65 70 75  
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80					85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380		385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395		400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
410		415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
425		430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
440		445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
455		460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
470		475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
485		490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
500		505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
515		520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
530		535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
545		550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
560		565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
575		580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
590		595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
605		610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
620		625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
635		640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
650		655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val

665					670					675				
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	Val	Pro
				680					685					690
Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys
				695					700					705
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
				710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe
				725					730					735
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln
				740					745					750
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu
				755					760					765
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr
				770					775					780
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro
				785					790					795
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile
				800					805					810
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg
				815					820					825
Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val			
				830					835					

<210> 254  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 254  
 agcccgtagca gaatctgctc ctgg 24

<210> 255  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 255  
 tgaagccagg gcagcgctct ctgg 24

<210> 256  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 256  
 gtacaggctg cagttggc 18

<210> 257  
 <211> 41  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-41  
 <223> Synthetic construct.

<400> 257  
 agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 258  
 gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259  
 <211> 4563  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 3635  
 <223> unknown base

<400> 259  
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 agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200  
 cgcccagacc gccgctagcg cgcgccgggc atgggtccct cttaaaggcg 250  
 caggccgagg cgggcgggggc ggggtgtgcg aacaaagcgc cggcgcgggg 300  
 cctgcggggc gctcgggggc cgcatgggc gcggcgggcc cgcgcgggcg 350  
 gcggcgctgc ccgggccggg cctcgcgggc ctagggcggg ctggcctccg 400  
 tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcggcggc 450  
 gggcgggcg gcggcccggc gggcggagcg gcgcgggcat ggccgcgcgc 500  
 ggccggcgcg cctggctcag cgtgctgctc gggctcgtcc tgggcttcgt 550  
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 gccacggcg ccgcgccagc ccgagggct gccggtccgg gcaggcgggc 650  
 gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgagctctg 700  
 gccgcccggc tcggaccag atggcgggcc gcgcgacagg aactttctct 750  
 tcgtgggagt catgaccgcc cagaaatacc tgcagactcg ggccgtggcc 800  
 gcctacagaa catggtccaa gacaattcct gggaaagttc agttcttctc 850  
 aagtgagggg tctgacacat ctgtaccaat tccagtagtg ccactacggg 900  
 gtgtggacga ctctacccg cccagaaga agtccttcat gatgctcaag 950  
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met	Ala	Ala	Arg	Gly	Arg	Arg	Ala	Trp	Leu	Ser	Val	Leu	Leu	Gly
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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg
				20					25					30

Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45

Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60

Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75

Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90

Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105

Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120

Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135

Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150

Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165

Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180

Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195

Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210

Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225

Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530					535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu
				560					565					570
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
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<210> 261

<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 261  
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<210> 262  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 262  
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<210> 263  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 263  
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<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
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gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
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tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys					
				65					70					75					
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				80					85					90					
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100					105					
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
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Leu Leu Lys Val Tyr  
350

<210> 266  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 266  
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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
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gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250  
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aggatttgct ttccagactcc agagcaaagt cagatgggta cagcctgtat 700  
gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750  
ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggtattga 800  
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<210> 267  
 <211> 466  
 <212> PRT  
 <213> Homo sapiens

<400> 267  
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Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
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His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
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Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
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Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
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Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
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Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
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Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
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Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
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Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
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Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
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Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
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Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
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Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
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His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
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Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
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Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

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 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

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 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaaatgc 300  
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 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
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<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
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 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
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 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
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 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
                     80                    85                    90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
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 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
                     110                    115                    120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
                     125                    130                    135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
                     140                    145                    150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
                     155                    160                    165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
                     170                    175                    180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
                     185                    190                    195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
                     200                    205                    210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
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Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
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Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
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Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271  
<211> 238  
<212> PRT  
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<400> 271  
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Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala  
35 40 45  
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys  
50 55 60  
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly  
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
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Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
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Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
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 <212> DNA  
 <213> Homo sapiens

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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu	35	40	45	
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe	50	55	60	
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile	65	70	75	
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu	80	85	90	
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys	95	100	105	
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met	110	115	120	
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser				

170										175					180				
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln					
				185					190					195					
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met					
				200					205					210					
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe					
				215					220					225					
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu					
				230					235					240					
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro					
				245					250					255					
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His					
				260					265					270					
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg					
				275					280					285					
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe					
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 <212> DNA  
 <213> Homo sapiens

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<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
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Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
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Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
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Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
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His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
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Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
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Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
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Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
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Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
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Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
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Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
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Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
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Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
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Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
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Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	260	265	270
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Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	335	340	345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	350	355	360
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Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	380	385	390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	395	400	405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	410	415	420
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<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens  
 <400> 277

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Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
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Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
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Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp
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Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu
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Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg
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Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
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agtaccacaa gacttggaga acttcattgc caagtttggg gactctgggt 950  
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000  
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 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100  
 atgtgaaaat tgtggactgg cttcctcaga gtgacctcct ggctcaccca 1150  
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200  
 catccagcat ggtgtgcca tgggtgggat ccctctcttt ggagaccagc 1250  
 ctgaaaacat ggtccgagta gaagccaaaa agtttgggtg ttctattcag 1300  
 ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350  
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcactcctgc 1400  
 gctccacccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450  
 gtccctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500  
 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550  
 tcaactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600  
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 ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900  
 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950  
 aaaatccacc ttccttctca tgcgcctctc cgaatcacac cctgactctt 2000  
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050  
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 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150  
 tgtgcttgag agttcagggc cggacacagg ctcacaggctc tccacattgg 2200  
 gtccctgtct ctggtgcca cagtgaagctc cttcttggct gagcaggcat 2250  
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 tctctcccca acctcactaa 2320

<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260					265					270				
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
				290					295					300
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser
				440					445					450
Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr
				455					460					465
Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp
				470					475					480
His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu
				485					490					495
Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala
				500					505					510
Val	Trp	Trp	Leu	Arg	Gly	Ala	Arg	Lys	Val	Lys	Glu	Thr		
				515					520					

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
tgcctttgct cacctacccc aagg 24

<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggt ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
gggctgttga tttgtggggg attttgaaga gaggagggaat aggaggaagg 50  
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cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc aggggtgccg cggtgagaat 400  
ccaggggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaagccac actggctacc 500  
 aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550  
 tgggggccgg gtgggccag gaggggtcag agcccgctct gctggagggg 600  
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 ggggccatct acttcgacca ggtcctgggtg aacgagggcg gtggctttga 800  
 ccgggcctct ggctccttcg tagccctgt ccgggggtgtc tacagcttcc 850  
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000  
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100  
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 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200  
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
 gagctgtggc atctccagac caggcctttc caccaccca ccccgagta 1300  
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350  
 ggcaaggttt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400  
 ctccggttcc cccaccccag cttcctgctc aatgctgac agggacaggt 1450  
 ggcgcagggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600  
 aggctcagcc acaggcagaa gggtggaag ggctggagt ctgtggctgg 1650  
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 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
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 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900



ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
 cactctgact gctgctcct tcctcccagc tctctcactg agttatcttc 2000  
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 gctgtcttat tctcctcctt aggcttccta ttacctggga ttccatgatt 2100  
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
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 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 287  
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser  
     1                    5                    10                    15  
 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly  
                     20                    25                    30  
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys  
                     35                    40                    45  
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly  
                     50                    55                    60  
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala  
                     65                    70                    75  
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn  
                     80                    85                    90  
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu  
                     95                    100                    105  
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val  
                     110                    115                    120  
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn  
                     125                    130                    135  
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val  
                     140                    145                    150  
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala  
                     155                    160                    165  
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgtctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50  
 tagccgcca gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200  
 ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250  
 agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300  
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350  
 tcacctggct caataggtcc aaggtggaaa agcagctaca ggtcatctca 400  
 gtgctccagt gggctctgtc cttccttgta ctgggagtgg cctgcagtgc 450  
 catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500  
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 aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600  
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650  
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 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750  
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800  
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 tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtggtcgg 900  
 ggggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950  
 tgcggaaccg caagggcttt gtgaaactgg ccctgcgtca tggagctgac 1000  
 ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050  
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 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250  
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 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350  
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400  
 tttgctctgt aaatttgga gtgtcatggg tgtctgtggg ttatttaaaa 1450  
 gaaattataa caattttgct aaacaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 293  
 gctgacctgg ttcccatcta ctcc 24

<210> 294  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 294  
 cccacagaca cccatgacac ttcc 24

<210> 295  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

<400> 296  
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50  
ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100  
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250  
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350  
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cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
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cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600  
gcgcttcgga gtgctgggga gtcceaaggt cctcgctaag aaggagctgc 650  
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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacaacta 2950  
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000  
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 accctgtctc 3060

<210> 297  
 <211> 368  
 <212> PRT  
 <213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	



Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	170	175	180
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	185	190	195
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	200	205	210
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	215	220	225
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	230	235	240
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	245	250	255
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	260	265	270
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	275	280	285
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	290	295	300
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	305	310	315
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	320	325	330
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	335	340	345
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	350	355	360
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								365		

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt ggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgctttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150  
tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200  
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250  
tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300  
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400  
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500  
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650  
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
gttgatatgg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
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 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900  
 cggtgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950  
 gccaggttg ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgata 1100  
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 gcggaggttg cagtgaagcc agatcaggcc actgtattcc aaccaggggtg 1300  
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 302  
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile  
 1 5 10 15  
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe  
 20 25 30  
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly  
 35 40 45  
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val  
 50 55 60  
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp  
 65 70 75  
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr  
 80 85 90  
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln  
 95 100 105  
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu  
 110 115 120  
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr  
 125 130 135  
 Cys Gly Val Leu Leu Ser Phe Leu

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100  
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200  
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
 ttctacccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350  
 ctctcgctgg agcagtggcc tcaccaactg tctcacgtct ggaggcactg 400  
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450  
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 ggcgatggct cccactggcc aggcattcagc cttgctgtag tcaatcactg 550  
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 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100  
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tgccctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
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 aattatggtt atttgtaa 1768

<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
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 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro  
 65 70 75  
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala  
 80 85 90  
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly  
 95 100 105  
 Arg Arg Arg Asp

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305

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 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200  
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 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550  
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 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850  
 caccttgccc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
				245					250					255	
Leu	Thr	Leu	Ala	Phe	Lys	Ile									
				260											

<210> 307  
 <211> 2272  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
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 gctaagatga agggctaccc tctaggcct gccaggatcg acgacatcgc 150  
 ggatggcgcc gtgaagcccc caccacaacaa gtaccccatc tttttctttg 200  
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
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 ggcagtgacg ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450  
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 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650  
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700



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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
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Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
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Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

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Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
				155					160					165
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
				170					175					180
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
				215					220					225
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
				230					235					240
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
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Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
				275					280					285
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
				290					295					300
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
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Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
				365					370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
				380					385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
				395					400					405
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
				410					415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
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Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
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				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
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Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
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<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu	35	40	45	
Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	50	55	60	
Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu	65	70	75	
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile				

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
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Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
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Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
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Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
				170					175					180					
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
				185					190					195					
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
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Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
				215					220					225					
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
				230					235					240					
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
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Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
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Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
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Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
				350					355					360					
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
				365					370					375					

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			



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Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu					
				680					685					690					
Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu					
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Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His					
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<220>  
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<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
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35 40 45  
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50 55 60  
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75  
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90  
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105  
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120  
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135  
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

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Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn					
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Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala					
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Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His					
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His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys					
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Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr					
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Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro					
				425					430					435					

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Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro		455	460	465
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala		470	475	480
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys		485	490	495
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp		500	505	510
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro		515	520	525
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val		530	535	540
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Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn		560	565	570
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Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys	830		835		

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctcctt cggtgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

<400> 321  
cagcagtggt ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50  
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgtttggta tcttggccct aactctaatt gtcctgtttt 200  
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcaactgatg 350  
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
gaccatgtat tggatcaatc cactctaatt atcagtttct gagttacaag 650  
actttgagga ggagggagaa gatcttcact ttcctgcaa cgaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750  
gaccgcgcac gccagacaag caagtgagga agaacttcca ataatgact 800  
atactgaaaa tggaaatagaa ttgatccca tgctggatga gagaggttat 850  
tggtgtattt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900  
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
tcactgtctg tgatcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000  
gggaggggtc aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050  
atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcactctg 1100  
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
 305 310 315

Arg Val

<210> 323  
 <211> 1174  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 gcggaactgg ctccggtggt cacctgagga gcggcgtgac cccgagggcc 50  
 caggagctg cccggtggc ctaggcaggc agccgcacca tggccagcac 100  
 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150  
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200  
 accaacaatcc tcacggcgt gtctacctg aaagggctct ggatggagtg 250  
 tgtgtggcac agcacaggca tctaccagt ccagatctac cgatccctgc 300  
 tggcgtgcc ccaagacctc cagggtgcc gcgcctcat ggtcatctcc 350  
 tgcctgtctc cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
 cacgcgtgc gccaaaggca caccgcaca gaccacctt gccatcctcg 450  
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500  
 tggaccacca acgacgtggt gcagaacttc tacaaccgc tgctgcccag 550  
 cggcatgaag tttgagattg gccaggcct gtacctgggc ttcattctct 600  
 cgtccctctc gctcattggt ggcacctgc tttgcctgtc ctgccaggac 650  
 gaggcaccct acaggcccta ccaggccccg cccagggccca ccacgaccac 700  
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750  
 gggccccctc agtgacctg gccacgcaca gcgggtacag gctgaacgac 800  
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850  
 gtccccggcg ggaactgtca tggaggcagg ggttcagca caaagtttac 900  
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950  
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
 atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttggga 1100  
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150  
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	



Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50  
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100  
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150  
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200  
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
 gacttcagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350  
 gtcctgggtg ccattggcct cctgggtatcc atctttgccc tgaaatgcat 400  
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450  
 ccgggatcat gttcattgtc tcagggtctt gtgcaattgc tggagtgtct 500  
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550  
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600  
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650  
 ggggggtgtga tgatgtgcat cgcctgccgg ggcctggcac cagaagaaac 700  
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
 aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta 850  
 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900  
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950  
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100  
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350  
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
 cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa 1450  
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500  
 tcttattaca gcaacaccat tctaggaggt tcctgagctc tccactggag 1550  
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600  
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850  
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100  
 aggttaaaac taattcttta a 2121

<210> 326  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile  
 1 5 10 15  
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp  
 20 25 30  
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln  
 35 40 45  
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe  
 50 55 60  
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met  
 65 70 75  
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
				245					250					255					
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50

gtagcagttc cggagtccag ctggctaaaa ctcattcccag aggataatgg 100

caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150

gtgggcacag tggctgtcac tgatcatgct cagtggagag tgcggcctt 200

cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250

tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300

tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggttt catgatggcc atccttggca 400  
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450  
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500  
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550  
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600  
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgct 650  
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850  
 caaagaaact ttgatttact gttcttaact gcctaactctt aattacagga 900  
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaccac aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taaggtyggt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta 1150  
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc cattttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450  
 ttaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650  
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaaca aaaaagttgt 1750  
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggttc tgtgaaaaat aaatttcctt cttgtaccat ttctgtttag 1850  
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900  
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
 aatgaatgtg ttctatttgc tttatacat tatattaata aattgtacat 2000  
 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
 tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50  
 ctgggctggg tgaatggcct ggtctcctgt gccctgccc tgtggaaggt 100  
 gaccgctttc atcggcaaca gcatcgtggg gcccaggtg gtgtgggagg 150  
 gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300  
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
 cgctgtgtgc tcacctctgg gattgtcttt gtcattctag gggctctgac 400  
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450  
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
 ttgggctggg cggcctcagg cttttgttg ctgggtgggg gggtgctgtg 550  
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600  
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 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
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 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800  
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 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
 cctctgtttc ctccgtctg ataagacgtc cccccccag ggccagggtc 1200  
 cagctatgta gacccccgcc cccacctcca acactgcacc cttctgccct 1250

gccccctcg tctaccccc ttacactca catttttatc aaataaagca 1360

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200  
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250  
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gcaagttcta tagctccttg ttggctctcc cgctgccct ggaaacagcc 350  
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400  
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ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500  
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tttctacaac ccagccatcc acataggta gaaacgagag ctgggagcag 600  
cacttttcct tggctgggca agcgtgctg tcctcttcat tggaggggg 650  
ctgctttgtg gatattgctg ctgcaacaga aagaagcaag ggtacagata 700  
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750  
caatgcttag taagacctcc accagttagt tctaagcct ccttttggct 800  
ccaagtatgg actatgggtc atgtttttta taaagtcctg ctagaaactg 850  
taagtatgtg aggaggaga acttgcttta tgtctagatt tacattgata 900  
cgaaagtttc aatttggtac tggtggtagg aatgaaaatg acttacttgg 950  
acattctgac ttcagggtga ttaaatgcat tgactattgt tggacccaat 1000  
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100  
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acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe



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Tyr Ser Ser Leu	Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg		
	20	25	30
Ala Leu Met Cys Val	Ala Val Ala Leu Ser Leu Ile Ala Leu Leu		
	35	40	45
Ile Gly Ile Cys Gly	Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
	50	55	60
Glu Arg Ala Lys Ala	Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
	65	70	75
Ile Leu Thr Gly Ile	Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
	80	85	90
Asn Ile Ile Ile Arg	Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
	95	100	105
Gln Lys Arg Glu Leu	Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
	110	115	120
Ala Ala Val Leu Phe	Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
	125	130	135
Cys Cys Asn Arg Lys	Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
	140	145	150
Tyr Arg Val Pro His	Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
	155	160	165
Ser Lys Thr Ser Thr	Ser Tyr Val		
	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
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 ctcaagaagct gctagtctgt ctcaaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200  
 tgtgggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250  
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 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400  
 ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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ctgctcgcgc cccgcgcgcca tggctgcctc cccgcgcgcg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggcgcgttg tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgagggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaa 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggtttctga 600

tttgccttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700  
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
1 5 10 15  
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser  
20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150  
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200  
gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300  
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350  
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400  
 gctacggctg aaattcctca atgattcaga gcagggtggc agggcctggc 450  
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500  
 cagcagggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550  
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600  
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650  
 cccggcccct cggggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
 ttcccctgac cgccactctg ggcttgccg gcttcaccct gtcctcagt 800  
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 agcgtcgccg gcccctccgg accttgctcc ccgcgccgcg gcgggagctg 900  
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 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050  
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 acgccaggtc ggtgggaggc tggtaaggg gagcggggag gggcagagga 1250  
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300  
 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
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Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
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 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700  
 ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatgggtt 750  
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 tggtatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 340  
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                   20                  25                  30  
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
                   35                  40                  45  
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
                   50                  55                  60  
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
                   65                  70                  75  
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
                   80                  85                  90  
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
                   95                  100                  105  
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
                   110                  115                  120  
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
                   125                  130                  135  
 Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.

<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 343  
atctcaggcg gcatcctgtc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24

<210> 345  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agcttttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
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actgagaacc caccagctca tcccagacac ctcatagcaa cctatattata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccgggggtaaa gggaggggaag caattcaatt tgaagtcct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtga gaagcaggtc 300  
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 agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctcgaactgt 1650  
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 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850  
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
 acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000  
 cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050  
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 acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300  
 gatttgtacc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350  
 tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400  
 aagagaatth tggccatcaa aatccagctc caagtgaacg taaagagctt 2450  
 atatatttca tgaagctgat ccttttgtgt gtgtgctcct tgtgttagga 2500  
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15

Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30

Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45

Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60

Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75

Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90

Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105

Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120

Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135

Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150

Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165

Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180

Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195

Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210

Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225

Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240

Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

545										550					555				
Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val					
				560					565					570					
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln					
				575					580					585					
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser					
				590					595					600					
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu					
				605					610					615					
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe					
				620					625					630					
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg											
				635															

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
 tatgtcgtg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351  
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ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100  
tcctctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcactct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtgc 200  
caggggagggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcactg cccccccagc cccccatca ggctttgagg agggggccgcc 350  
ctcatcccaa taccctggg ctatcgtgtg gggtcaccac gtgtctcgag 400  
aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggg 450  
tttgagccc ctcatgggct cgcaaccca caccctaact cagactccat 500  
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600  
gtcacaatta ccactccat catcattgtt ctctgggcca ctggcatcat 650  
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700  
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750  
tccccggctg gagtcaactgt gctggggggc ttcggggact cacctacccc 800  
caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850  
acccaagggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900  
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950  
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ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350  
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 cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450  
 cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500  
 cacccttggtg cactcacatg aaagccttgc aactcacct ccaccttcac 1550  
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 tcgggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctcccca 1900  
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 tctgacagat ggggttttggg gagtcgcctg ctgcactaca tgagaaaggg 2050  
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 aagtctaccc ttcccttccc ggactccctc ctgtccctc ctttctccc 2300  
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 caggttcttc cctccttctc actggttttt ccaccttcct ccttcccttc 2400  
 ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450  
 ttcttgggt gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500  
 tcaaataaag cctttgcaag ataa 2524

<210> 352  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
 1 5 10 15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35					40					45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50					55					60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65					70					75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80					85					90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95					100					105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110					115					120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125					130					135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230					235					240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg cctcactcc 50

cggccaggat ggcatacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcggtcgc tggggcccg cgctatcgcg gccatcgtga 350  
 tcgccgcct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5					10					15

Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30

Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45

Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60

Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75

Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90

Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105

Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttggt tggcgcgagg ctgaagggtg tggcgcgagg agcgctgttg 50

gttgccggc ggcgggccgg gacgggcatg gccctgctgc tgtgctggt 100



gtgcctgacg gggcgctgg cccacggctg tctgcactgc cacagcaact 150  
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200  
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300  
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
 taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400  
 catcttcggg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
 acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500  
 agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
 agtagcccc agaggcgctg ggagtgttg caccgccctc cctgaagtt 600  
 tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggccc 650  
 atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
 tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
 acgtcgcctg ctttggtat aactgcgagt agggctcagg catcacaccc 800  
 acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
 gggctccccg ccttcacct ggctgtcatc gggtagggcg gggccgtggg 900  
 ttcaggggcg caccacttc aagcctgtgt cccacaggct ctcggcgag 950  
 tggaagtcag ctgtccagg cctcctgaac tacataaata actggcacia 1000  
 gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
 cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcccacgtc 1100  
 ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150  
 ggggtgcag tccttttct cctcaaagg ctccgacct cagctggagg 1200  
 cgggcatctt tcctaaagg tcccatagg gtctggttcc acccatccc 1250  
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 acccatgtgg tggtttcatg aacagaccac gtcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaagggga 1600  
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
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 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
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 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

Ser Pro Arg Gly Asp Leu Pro  
155

<210> 357  
<211> 1536  
<212> DNA  
<213> Homo sapiens

<400> 357  
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cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100  
ttgagaaatc ctcatgtgtt cctgggtgctg cccaggaacc cacgtggctc 150  
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250  
gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350  
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
tcagattcat ctctcctga taatgaacaa ggcctccca gagtatgaag 550  
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
ctctttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650  
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700  
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750  
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
aactcaaatc tcagagacac taaacaacag gatcactagg cctgccacc 950  
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100  
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
tcaaaaaacca aaggatggtt ttaaaccact ttgtgaaatt gtctttttgc 1400  
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450  
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaatcaa 1500  
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 359  
 ccagcagtgc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
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cctcagcggg gaccgggct caggacgcg gcggcggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250  
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ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcggttga cctcagcttc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
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tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900  
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tgcgatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100  
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 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
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 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

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Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90
Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95					100					105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcg ccccggcgca gtcccccgcg gccccgacc ctgaggcgtc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccg 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

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cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
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agattactga tttcccatTT aagtgggaatt cgtcattatg aaaaggacat 700  
aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
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gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850  
ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900  
tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
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ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050  
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caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150  
cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200  
aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatTTtgg 1250  
gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300  
catgtttata aagtaaaaaa a 1321

<210> 366  
<211> 373  
<212> PRT  
<213> Homo sapiens

<400> 366  
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
1 5 10 15  
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
20 25 30  
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
35 40 45  
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
50 55 60  
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
65 70 75  
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370	

<210> 367

<211> 30  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-30  
<223> Synthetic construct.

<400> 367  
tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggtt cattctcctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
aaaacctcag aacaactcat tttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac cgggctgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
 tcaactgctct ggaaccagca ggatgggtacc ttgtccctgt cacagcggca 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
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 gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700  
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 agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
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Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373  
 <211> 1706  
 <212> DNA  
 <213> Homo sapiens

<400> 373  
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 cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150  
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250  
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 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
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 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
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 tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200  
 cagcatgagc ttcctacgga gaaaggtgat ccctgagaca gagcaggctg 1250  
 gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300  
 ctcttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
 cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400  
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
 gaggagccct atgccctga gctgtaacct cactccagga caagatagct 1500  
 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaaggctc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaaata gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Artificial

<400> 375  
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50  
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100  
 gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgcccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250



ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350  
 ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaccca ggcacagct gacatccccg cctcttctct gctcggccga 500  
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgagaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800  
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
 cccaggggt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawtnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110						115					

<210> 379  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 379  
 ctgcctccac tgctctgtgc tggg 24

<210> 380  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 380  
 cagagcagtg gatgttcccc tggg 24

<210> 381  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ctttctggat gggggcccag gggggcccagg agagtataaa 50  
ggcgtatgtg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100  
gccctgggat gcaccggcca gagggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gccccacctg ggcaggggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttggg 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggatatggc atgtacacca gcaaggaccg ctatttctat 450  
tttggaagc ttgatggcca gatctcctct gcctaccca gccaagaggg 500  
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcataaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
ggtatggggc catccgagct gagggcatct gtgtgggtgt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5					10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50  
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100  
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttcctaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400  
 tgtcagcgag cctgactca ctacagtgc gctgacagg gctgtcatgc 450  
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550  
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactctgct gggtgcttag 700  
 gtttgcctt togtataaac agccttcaaa aacttaagta taatcaattt 750  
 aaagggtca accagctcac ctggctatac cttgaccata accatatcag 800  
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950  
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000  
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
 aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100  
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagacct 1200  
 cagaaccttt acttgcagtg gaataaaatc agtgtcatag gacagaccat 1250  
 gtcctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300  
 tcgaagcttt cagtggacc agtggtttcc agtgtgtccc gaatctgcag 1350  
 cgcctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400  
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaa 1500  
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
 agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
 ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650  
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgac 1700  
 ggtgggagcc acagagccc gcccagagac cgatgctgac gccgagcaca 1750  
 tctctttcca taaaatcacc gcgggcagcg tggcgctttt cctgtccgtg 1800  
 ctgctcatcc tgctggttat ctacgtgtca tggaagcgg accctgcgag 1850  
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac agggaaaaga 1900  
 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950  
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
 gggaccctgc acctataaca aatcgggtc caggagtggt gaggtatgaa 2050  
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtcttta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150  
 tctccctctc actttggtgg caagatcctt ccttgtcggt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

	200		205		210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe			
	215		220		225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys			
	230		235		240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu			
	245		250		255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly			
	260		265		270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu			
	275		280		285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser			
	290		295		300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu			
	305		310		315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe			
	320		325		330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu			
	335		340		345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile			
	350		355		360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu			
	365		370		375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu			
	380		385		390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly			
	395		400		405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile			
	410		415		420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu			
	425		430		435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys			
	440		445		450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys			
	455		460		465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr			
	470		475		480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu			
	485		490		495



Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
500 505 510

Cys Glu Val

<210> 386  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 386  
ctgggatctg aacagtttcg gggc 24

<210> 387  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 387  
ggtccccagg acatggtctg tccc 24

<210> 388  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 388  
gctgagtta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
<211> 1449  
<212> DNA  
<213> Homo sapiens

<400> 389  
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100  
gcatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
ctcggacctc ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250  
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300  
 gagaccccca attgattctc acaggcgcac catggcagtt tttgctgttg 350  
 gagacttgga ctctatztat gggacagaag cagctgtgag tccaactggt 400  
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcctgctcc 450  
 atgttttggc cctttaggct cccacactcc atatgaagaa attgtaaaaa 500  
 caactgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
 tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaaagaat 650  
 ggatgttga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700  
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
 attaagtctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
 tctgctttaa actctttcct agcatggggt ccataaaaaat tattataatt 900  
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
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 ctccatagtc catagtgttt ctctggagcc tcagggccttg gcatttattg 1250  
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
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<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
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Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
			80						85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140						145						

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 391  
 cttttcagtg tcacctcagc gatctc 26

<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 392  
 ccaaaacatg gagcaggaac agg 23

<210> 393  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 394  
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gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctcttctac tttgggagag agagaaagtc agatgccoct tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttggt gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatttggg 500  
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaa atactagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750  
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cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850  
ttgaaaatca ccttggtgctg ctccatccac tgtggattat atcctatggc 900  
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950  
aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aattttaaag ttatttggtt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

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agtatataac acgttttttg gacaagtga gaatgtttta tcattctgtc 1250  
atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300  
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350  
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acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10					15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
                             20                            25                            30  
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
                             35                            40                            45  
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
                             50                            55                            60  
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
                             65                            70                            75  
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
                             80                            85                            90  
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
                             95                            100                            105  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
                             110                            115                            120  
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
                             125                            130                            135  
 Ser Gly Ser Ile Arg  
                             140

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
 cgcgccggg cgcgcggggg gagcgtgccg aggcggctgt ggcgcaggct 50  
 tccagcccc accatgccgt ggccctgct gctgctgctg gccgtgagt 100  
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 acctcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
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 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcacccactg ctttctcccc ctttcgctac ctggagtcgc 400  
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 atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750  
 ggccttacac acctgtctct gccagcctg cagaggctcc ctgagctggc 800  
 gccagtggc ttccgtgagc taccgggcct gcaggctctg gacctgtcg 850  
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gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400  
tttgttact tttgtaatat tgcctgggc ctgtgttggg gtgttgggg 2450  
aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500  
ccccacagg cagtgagctc tgtcttcccc cacctgccta gcccatcatc 2550  
tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln	1	5	10	15
Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr	20	25	30	
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser	35	40	45	
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr	50	55	60	
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu	65	70	75	
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp	80	85	90	
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser	95	100	105	
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	110	115	120	
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	125	130	135	
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	140	145	150	



Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu	Ser
	155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
	170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
	185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
	200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
	215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
	230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
	245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
	260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
	275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
	290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
	305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
	320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
	335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu		
	350		

<210> 398  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 398  
 ccctgccagc cgagagcttc acc 23

<210> 399  
 <211> 23  
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

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gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

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aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

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 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 402  
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 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu  
 20 25 30  
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys  
 35 40 45  
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
 50 55 60  
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu  
 65 70 75  
 Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser  
 80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 403  
 ctccctgtggt ctccagattt caggccta 28

<210> 404  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
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aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc ggggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcgcat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat ggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcagc gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttctgg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-31  
<223> Synthetic construct.

<400> 407  
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-34  
<223> Synthetic construct.

<400> 408  
gcggaattct taaaatggac tgactccact catc 34

<210> 409  
<211> 1487  
<212> DNA  
<213> Homo sapiens

<400> 409  
cggacgcgtg ggcgcggggac gccggcaggg ttgtggcgca gcagtctcct 50  
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100  
cagcatttaa tgaaaaatct atgcttaaga agtaaaaatg gcaggcttcc 150  
tagataatct tcgttgccca gaatgtgaat gtattgactg gaggtagaga 200  
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250  
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300  
accatgcctt tcacacatgt ggtgtatctt ccacattggc tttcttcatt 350  
ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400  
ctgttttagga agaacaggtg ctgcagtttg gcttttcatt ggtttcattg 450  
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtcatat 500  
gttaccctaaa atactgatgt ttatccggga ctactgtgtg tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700  
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
 tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900  
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950  
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000  
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100  
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
 aggttgcagt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200  
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
 tttatataat gattttttta atgccc aaag gactagtttg aaagcttctt 1450  
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75



Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe  
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr  
155

<210> 411  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 411  
gtttgaggaa gctgggatac 20

<210> 412  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 412  
ccaaactcga gcacctgttc 20

<210> 413  
<211> 40  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 413  
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100  
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350  
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
catgaaaacc atccgtctgc cagctgggtt ggcagcctcg cccaccaagg 450  
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500  
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550  
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600  
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650  
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700  
gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750  
acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800  
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850  
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900  
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000  
ttcctcagcc aggggcctga agaagtcctt gcctgactta ggagtcagag 1050  
cccggcaggg gctgaggagg aggagcaggg ggtgctgctt ggaaggtgct 1100  
gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaaccc 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala  
   1                  5                  10                  15  
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
                   20                  25                  30  
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
                   35                  40                  45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
                   50                  55                  60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
                   65                  70                  75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
                   80                  85                  90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
                   95                  100                  105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
                   110                  115                  120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
                   125                  130                  135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
                   140                  145                  150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
                   155                  160                  165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
                   170                  175                  180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
                   185                  190                  195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
                   200                  205                  210  
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
                   215                  220

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-21  
 <223> Synthetic construct.  
  
 <400> 416  
 gccatagtca cgacatggat g 21  
  
 <210> 417  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 417  
 ggatggccag agctgctg 18  
  
 <210> 418  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
 aaagtacaag tgtggcctca tcaagc 26  
  
 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
 tctgactcct aagtcaggca ggag 24  
  
 <210> 420  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
 attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200  
ctctctctct gctgtccta gtctcttagt cctcaaattc ccagtcccct 250  
gcaccccttc ctgggacact atgttggttct ccgccctcct gctggagggtg 300  
at ttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgocca gctccacctg 600  
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900  
cgctacaatg gctcgetcac aactccccct tgctaccaga gtgtgctctg 950  
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
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attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250  
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ccttcccctg gacatctctt agagaggaat ggaccaggc tgcattcca 1450  
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550  
gaagtttggg atatacccca aagtctctta cccctcact tttatggccc 1600  
tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650  
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t 1701

<210> 423  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
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Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
20 25 30  
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
35 40 45  
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
50 55 60  
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
65 70 75  
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala					
				95					100					105					
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
				110					115					120					
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
				125					130					135					
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
				140					145					150					
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
				155					160					165					
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
				170					175					180					
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
				185					190					195					
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
				200					205					210					
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
				215					220					225					
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
				230					235					240					
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
				245					250					255					
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
				260					265					270					
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
				275					280					285					
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
				290					295					300					
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
				305					310					315					
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
				320					325					330					
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
				335															

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 424  
gtaaagtcgc tggccagc 18

<210> 425  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 425  
cccgatctgc ctgctgta 18

<210> 426  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 426  
ctgcactgta tggccattat tgtg 24

<210> 427  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 427  
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
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acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150



aacctgcttt gggactccct cccacaaaac tggtccgga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300  
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gacctggga 350  
 gggttgaatg tacaacagca actgcacca catgtgttac caatTTTTgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcattctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
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 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	80	85	90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	95	100	105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	110	115	120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	125	130	135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	140	145	150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	155	160	165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	170	175	180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	185	190	195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		200	205	

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 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

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 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150  
 gccccgcgc ctccccgcag cggctccgcg gectctgtct gctcctgtctg 200  
 ctgcagctgc ccgcgccgtc gagcgcctct gagatcccca aggggaagca 250  
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350  
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600  
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700  
 aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750  
 gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800  
 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
 tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctctttt 900  
 ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt 1000  
 tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
 aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
 acattctctc aacctataat ttggaatatt gttgtggtct tttgttttt 1150  
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
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 tccaaca 1257

<210> 431  
 <211> 243  
 <212> PRT  
 <213> Homo Sapien

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 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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Leu Pro Lys

<210> 432  
 <211> 18  
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<220>  
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<400> 432  
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<210> 433  
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<220>  
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<210> 434  
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<400> 434  
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<210> 435

<211> 19  
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 <400> 435  
 cccacctgta ccacatgt 19  
  
 <210> 436  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <210> 437  
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<400> 440  
gggtcgtgtt ttggagaga 19

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<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
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<400> 443  
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<210> 444  
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<400> 444  
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 ccctagctga ccccttca 18

<210> 451  
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 <210> 455  
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 <210> 457  
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 <210> 458  
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 <400> 458  
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 <210> 460  
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 <210> 461  
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<400> 461

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<210> 462

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<210> 463

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

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<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gccagagtc ccacttgt 18

<210> 468

<211> 19

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<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

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<213> Artificial Sequence

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cgagtgtgtg cgaaacctaa 20

<210> 472

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